

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 29, 2004, 09:05:16 ; Search time 21 Seconds
 (without alignments)

590.750 Million cell updates/sec

Title: US-09-726-899-3

Perfect score: 678

Sequence: 1 MSFPKYKPSSLRLTPETLDP.....DRKEKLIQEKGKLDRTFHLSY 129

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 9616682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_76:*

1: P1c1:*

2: P1c2:*

3: P1c3:*

4: P1c4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	6.78	100.0	129	2	JB0383		NADH2 dehydrogenase (ubiquinone) (BC 1.6.5.3) chain B15 - human
2	51.4	75.8	129	2	S28237		NADH2 dehydrogenase (ubiquinone) (BC 1.6.5.3) chain B15 - bovine
3	31.5	46.5	133	2	JC2003		NADH2 dehydrogenase (ubiquinone) (BC 1.6.5.3) chain B15 - cattle
4	14.9	22.0	179	2	A3164		NADH2 dehydrogenase (ubiquinone) (BC 1.6.5.3) chain B15 - horse
5	88.5	13.1	1078	2	S77162		NADH2 dehydrogenase (ubiquinone) (BC 1.6.5.3) chain B15 - cow
6	82	12.1	757	2	AB0083		NADH2 dehydrogenase (ubiquinone) (BC 1.6.5.3) chain B15 - dog
7	7.4	10.9	308	2	G83104		NADH2 dehydrogenase (ubiquinone) (BC 1.6.5.3) chain B15 - dog
8	7.4	10.9	451	2	F75177		NADH2 dehydrogenase (ubiquinone) (BC 1.6.5.3) chain B15 - dog
9	70.5	10.4	788	2	S75209		NADH2 dehydrogenase (ubiquinone) (BC 1.6.5.3) chain B15 - dog
10	70	10.3	420	2	A10921		NADH2 dehydrogenase (ubiquinone) (BC 1.6.5.3) chain B15 - dog
11	70	10.3	695	2	G64327		NADH2 dehydrogenase (ubiquinone) (BC 1.6.5.3) chain B15 - dog
12	70	10.3	1025	2	T18376		NADH2 dehydrogenase (ubiquinone) (BC 1.6.5.3) chain B15 - dog
13	69.5	10.3	294	2	S22440		NADH2 dehydrogenase (ubiquinone) (BC 1.6.5.3) chain B15 - dog
14	69	10.3	328	2	B95404		NADH2 dehydrogenase (ubiquinone) (BC 1.6.5.3) chain B15 - dog
15	69	10.2	298	2	S69523		NADH2 dehydrogenase (ubiquinone) (BC 1.6.5.3) chain B15 - dog
16	69	10.2	1023	2	S12519		NADH2 dehydrogenase (ubiquinone) (BC 1.6.5.3) chain B15 - dog
17	69	10.2	1660	2	T18561		NADH2 dehydrogenase (ubiquinone) (BC 1.6.5.3) chain B15 - dog
18	68.5	10.1	294	2	S23095		NADH2 dehydrogenase (ubiquinone) (BC 1.6.5.3) chain B15 - dog
19	68.5	10.1	294	2	T49271		NADH2 dehydrogenase (ubiquinone) (BC 1.6.5.3) chain B15 - dog
20	68.5	10.1	574	2	S57072		NADH2 dehydrogenase (ubiquinone) (BC 1.6.5.3) chain B15 - dog
21	68.5	10.1	921	2	P84593		NADH2 dehydrogenase (ubiquinone) (BC 1.6.5.3) chain B15 - dog
22	68.5	10.1	1333	2	A36373		NADH2 dehydrogenase (ubiquinone) (BC 1.6.5.3) chain B15 - dog
23	68.5	10.1	1333	2	T38401		NADH2 dehydrogenase (ubiquinone) (BC 1.6.5.3) chain B15 - dog
24	68	10.0	185	2	S12205		NADH2 dehydrogenase (ubiquinone) (BC 1.6.5.3) chain B15 - dog
25	68	10.0	716	1	JC5061		NADH2 dehydrogenase (ubiquinone) (BC 1.6.5.3) chain B15 - dog
26	67.5	10.0	153	1	WMVQBY		NADH2 dehydrogenase (ubiquinone) (BC 1.6.5.3) chain B15 - dog
27	67.5	10.0	289	2	E75391		NADH2 dehydrogenase (ubiquinone) (BC 1.6.5.3) chain B15 - dog
28	67.5	10.0	296	2	C82645		NADH2 dehydrogenase (ubiquinone) (BC 1.6.5.3) chain B15 - dog
29	67.5	10.0	600	2	C83142		NADH2 dehydrogenase (ubiquinone) (BC 1.6.5.3) chain B15 - dog

ALIGNMENTS

RESULT 1	JB0383	NADH2 dehydrogenase (ubiquinone) (BC 1.6.5.3) chain B15 - human
C;Species: Homo sapiens (man)		
C;Accession: JE0383		
C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 03-Jun-2002		
R;Loeffer, J. L.C.M.; Triepels, L.P.; van den Heuvel, R.H.; Buskens, C.A.F.		
Biochem. Biophys. Res. Commun. 253, 415-422, 1998		
A;Title: cDNA of eight nuclear encoded subunits of NADH:ubiquinone oxidoreductase: Hume A;Reference number: JE0379; MUID:9907250; PMID:9878551		
A;Status: preliminary		
A;Molecule type: mRNA		
A;Accession: JE0383		
Query Match 100.0%; Score 678; DB 2; Length 129;		
Best Local Similarity 100.0%; Pred. No. 8.5e-65;		
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Query 1 MSFPKYKPSSLRLTPETLDPDAEYNNSPETRAQARLRAIQLKREYLQYNDPNRQLI 60		
Db 1 MSFPKYKPSSLRLTPETLDPDAEYNNSPETRAQARLRAIQLKREYLQYNDPNRQLI 60		
Qy 61 ENPALLRWAYARTINVPNFRPTPKNSLMGALCGPLIFTYYIKTERDEKEKLQEQK 120		
Db 61 ENPALLRWAYARTINVPNFRPTPKNSLMGALCGPLIFTYYIKTERDEKEKLQEQK 120		
Qy 121 LDRTPHLSY 129		
Db 121 LDRTPHLSY 129		
Qy 121 LDRTPHLSY 129		
Db 121 LDRTPHLSY 129		

RESULT 2

S28237

NADH2 dehydrogenase (ubiquinone) (BC 1.6.5.3) chain B15 - bovine

C;Species: Bos primigenius taurus (cattle)

C;Accession: S28237

C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 03-Jun-2002

R;Walker, J.E.; Arizmendi, J.M.; Dupuis, A.; Fearnley, I.M.; Finel, M.; Medd, S.M.; Pil

J. Mol. Biol. 226, 1051-1072, 1992

A;Title: Sequences of 20 subunits of NADH: ubiquinone oxidoreductase from bovine heart

A;Reference number: S28237; MUID:92389317; PMID:1518044

A;Accession: S28237

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-129 <LOB>

A;Cross-references: GB:AF044957; NID:94164445; PID:94164446

C;Keywords: NADH2 oxidoreductase

Result	Score	Query	Match	Length	DB	ID	Description
1	673	99.3	128	1	NBSM_HUMAN		095168 homo sapien
2	509	75.1	128	1	NBSM_BOVIN		P48305 bos taurus
3	315	46.5	133	1	NBSM_CHICK		P48306 gallus gallus
4	88.5	13.1	1078	1	GRB_STNY3		P77966 synchocyst
5	74	10.9	451	1	TRB2_PTYRA		Q9V150 pyrococcus
6	71	10.5	270	1	PGC_ZYMMO		Q9X3X1 zymomonas m
7	70.5	10.4	771	1	DNK3_STNY3		P73098 synchocyst
8	70	10.3	384	1	SYX18_HUMAN		P35713 homo sapien
9	70	10.3	420	1	WCCC_SALTI		P92389 salmonella
10	70	10.3	695	1	VATI_METJA		Q57675 methanococc
11	69.5	10.3	294	1	CC21_ORYZA		P29618 oryza sativ
12	69	10.2	298	1	VPO_BPHIP1		P51719 bacteriophaga
13	69	10.2	656	1	MTHR_HUMAN		P42898 homo sapien
14	69	10.2	759	1	SC633_HUMAN		Q9ugp8 homo sapien
15	69	10.2	759	1	SC633_MOUSE		Q8vhe0 mus musculus
16	69	10.2	1023	1	GJL_DRONB		P33438 drosophila
17	69	10.2	1660	1	VITG6_OSCBRR		Q94637 oschreiter
18	68.5	10.1	294	1	CC2A_ARATH		P24100 arabidopsis
19	68.5	10.1	574	1	BPA1_YEAST		P47113 saccharomyces
20	68.5	10.1	1333	1	RT21_SCIPPO		Q05654 schizosaccharomyces
21	68.5	10.1	1333	1	RP22_SCIPPO		Q9Cr22 schizosaccharomyces
22	68.5	10.1	1333	1	RT23_SCIPPO		Q9ur07 schizosaccharomyces
23	68	10.0	270	1	LPSC_RHIME		Q9rgm9 rhizobium m
24	67.5	10.0	153	1	VPG_EYDWP		P09513 barley yellows virus
25	67	9.9	232	1	NEBP1_PTYRA		Q9v0m0 pyrococcus
26	67	9.9	455	1	PX5_RAT		P51578 rattus norvegicus
27	67	9.9	618	1	M3K2_HUMAN		Q9Y2us homo sapiens
28	66.5	9.8	1036	1	SBECA_SPIOL		Q36795 spinacia ol
29	66	9.7	193	1	LOLB_NELIMA		P57023 nelssonia
30	66	9.7	406	1	VPS_FSIINU		Q9B1x9 psilotum nudum
31	66	9.7	420	1	WCC_SALTY		Q91649 salmonella
32	66	9.7	657	1	VPA4_POWPV		P17355 fowlpox virus
33	66	9.7	677	1	RN14_YEAST		P25298 saccharomyces

ALIGNMENTS

Scoring table:	BLOSUM62
Gapop:	10.0 , Gapext: 0.5
Searched:	127863 seqs, 47026705 residues
Total number of hits satisfying chosen parameters:	127863
Minimum DB seq length:	0
Maximum DB seq length:	2000000000
Post-processing: Minimum Match 0%	
Maximum Match 100%	
Listing First 45 summaries	
Database :	SwissProt_41::

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

3

RESULT 1							
NBSM_HUMAN	ID_NBSM_HUMAN	STANDARD;	PRT;	128 AA.			
AC	095168;						
DT	15-JUL-1999 (Rel. 38, Created)						
DT	15-JUL-1999 (Rel. 38, Last sequence update)						
DT	15-SEP-2003 (Rel. 42, Last annotation update)						
DE	NADH-ubiquinone oxidoreductase B15 subunit (EC 1.6.5.3) (EC 1.6.99.3)						
DB	(Complex I-B15) (CI-B15)						
GN	NDUFB4.						
GN	Homo sapiens (Human)						
OC	Eukaryota; Metasoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Cattarrhini; Hominidae; Homo.						
OC	NCBI_TaxID:9606;						
RN							
RP	SEQUENCE FROM N.A.						
RX	Medline=99097250; PubMed=9878551;						
RA	Loefzen J.L.C.M., Triepels R.H., van den Heuvel L., Schuslik M.,						
RA	Buskens C.A.P., Smeets R.J.P., Trijbels J.M.P., Smeitink J.A.M.;						
RA	"cDNA of eight nuclear encoded subunits of NADH:ubiquinone oxidoreductase: human complex I cDNA characterization completed."						
RA	[1]						
RA	SEQUENCE FROM N.A.						
RA	Medline=22388257; PubMed=12477932;						
RA	Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,						
RA	Schuler G.D., Klausner R.D., Collins F.S., Wagner B.A., Shemesh L., Shemesh C.M., Bhat N.K.,						
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,						
RA	Hopkins R.F., Jordan R., Moore T., Max S.I., Wang J., Hsieh F.,						
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Longellano N.A., Peters G.J., Abramson R.D., Mullany S.J., Bosak S.A., McElroy P.J., McKernan K.J., Malek J.A., Gunnarsson P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalona D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C., Rodriguez A.C., Grimwade J., Schmitz J., Myers R.M., Butfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schenck A., Scheiner A., Jones S.J.M., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences";						
RA	Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903 (2002).						
RA	Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C., Rodriguez A.C., Grimwade J., Schmitz J., Myers R.M., Butfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schenck A., Scheiner A., Jones S.J.M., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences";						
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RA	Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C., Rodriguez A.C., Grimwade J., Schmitz J., Myers R.M., Butfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schenck A., Scheiner A., Jones S.J.M., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences";						
RA	Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903 (2002).						
RA	Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C., Rodriguez A.C., Grimwade J., Schmitz J., Myers R.M., Butfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schenck A., Scheiner A., Jones S.J.M., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences";						
RA	Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903 (2002).						
RA	Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C., Rodriguez A.C., Grimwade J., Schmitz J., Myers R.M., Butfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schenck A., Scheiner A., Jones S.J.M., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences";						
RA	Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903 (2002).						
RA	Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C., Rodriguez A.C., Grimwade J., Schmitz J., Myers R.M., Butfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schenck A., Scheiner A., Jones S.J.M., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences";						
RA	Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903 (2002).						
RA	Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C., Rodriguez A.C., Grimwade J., Schmitz J., Myers R.M., Butfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schenck A., Scheiner A., Jones S.J.M., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences";						
RA	Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903 (2002).						
RA	Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C., Rodriguez A.C., Grimwade J						

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DR EMBL; AP044957; AA05421.1; .
DR PIR; JEB0383; JEB0383.
DR Gene; HGNC; 7639; NDUFB4.
DR MIM; 603840; .
DR GO; GO:0005748; C: NADH dehydrogenase complex (ubiquinone) (se. . .) TAS.
DR GO; GO:0008137; P: NADH dehydrogenase (ubiquinone) activity; TAS.
DR GO; GO:005120; P: oxidative phosphorylation, NADH to ubiquinone; TAS.
KW Oxidoreductase; NAD; Ubiquinone; Mitochondrion; Acetylation.
FT INIT_MET 0
FT MOD_RES 1
FT SEQUENCEB 128 AA; 15077 MW; DCCPGBPRA6F99N8 CRC64;
SQ Query Match 99.3%; Score 673; DB 1; Length 128;
Best Local Similarity 100.0%; Pred. No. 1.3e-62; Indels 0; Gaps 0;
Matches 128; Conservative 0; Mismatches 0; Gaps 0;
Db 1 SPFPKYPSLRLTPETIDPAEYNISPETRRAQERLARAQKREYLLQINDPNRGLIE 61
Db 2 SPFPKYPSLRLTPETIDPAEYNISPETRRAQERLARAQKREYLLQINDPNRGLIE 61
Qy 62 NPALLRWAAYARTINVPNFRTPKNSLGMALCGPGPFLIIFYTIIKTERDRKEKLQIEGKL 121
Db 61 NPALLRWAAYARTINVPNFRTPKNSLGMALCGPGPFLIIFYTIIKTERDRKEKLQINDPNRGLIE 60
Qy 122 DRTFHLSY 129
Db 121 DRTFHLSY 128

RESULT 2
NBSM_BOVIN STANDARD; PRT; 128 AA.
AC P48305
DT 01-FEB-1996 (Rel. 33, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DB NADH-ubiquinone oxidoreductase B15 subunit (EC 1.6.99.3) (Complex I-B15) (CI-B15).
GN NDUFB4.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Phasianinae; Galliformes; Gallus.
OC Bovidae; Bovinae; Bos.
RN [1] NCBI_TaxID=9913;
RN [1] SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RN RP SEQUENCE FROM N.A.
RX TISSUE=Heart;
RX MEDLINE=92389317; PubMed=1518044;
RA Walker J.B.; Arizmendi J.M.; Dupuis A.; Pearnley I.M.; Finel M.,
RA Medd S. M.; Pilkington S.J.; Runswick M.J.; Skeel J.M.;
RT "Sequences of 20 Subunits of NADH:ubiquinone oxidoreductase from
RT bovine heart mitochondria. Application of a novel strategy for
RT sequencing proteins using the polymerase chain reaction.",
RL J. Mol. Biol. 226:1051-1072(1992).
CC - FUNCTION: TRANSFER OF ELECTRONS FROM NADH TO THE RESPIRATORY
CC CHAIN. THE IMMEDIATE ELECTRON ACCEPTOR FOR THE ENZYME IS BELIEVED
CC TO BE UBIQUINONE (BY SIMILARITY).
CC - CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
CC - CATALYTIC ACTIVITY: NADH + acceptor = NAD(+) + reduced acceptor.
CC - SUBUNIT: COMPLEX I IS COMPOSED OF ABOUT 40 DIFFERENT SUBUNITS.
CC - SUBCELLULAR LOCATION: Mitochondrial inner membrane; matrix side.

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CC or send an email to licensee@ebi.ac.uk).

CC DR EMBL; X64898; CAA46107.1; .
DR PIR; S28237; S28237.
KW Oxidoreductase; NAD; Ubiquinone; Mitochondrion; Acetylation.
FT INIT_MET 0
FT MOD_RES 1
SQ SEQUENCE: 128 AA; 15053 MW; CC1323B9880DF7D5 CRC64;
Qy 75.1%; Score 509; DB 1; Length 128;
Best Local Similarity 73.4%; Pred. No. 1.1e-45;
Matches 94; Conservative 18; Mismatches 16; Indels 0; Gaps 0;
Db 2 SPFPKYPSLRLTPETIDPAEYNISPETRRAQERLARAQKREYLLQINDPNRGLIE 61
Db 1 SPFPKYPSLRLTPETIDPAEYNISPETRRAQERLARAQKREYLLQINDPNRGLIE 60
Qy 62 NPALLRWAAYARTINVPNFRTPKNSLGMALCGPGPFLIIFYTIIKTERDRKEKLQIEGKL 121
Qy 61 DPALAVRWTYARSANIVENFRPNTKSILGALPGIPLVWYTFKTDKREKLQIEGKL 120
Db 122 DRTFHLSY 129
Db 121 DRTFHLSY 128

RESULT 3
NBSM_CHICK STANDARD; PRT; 133 AA.
AC P48306
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Putative NADH-ubiquinone oxidoreductase B15 subunit (EC 1.6.5.3)
DE (BCI 1.6.99.3) (Complex I-B15) (CI-B15) (Hypothetical protein Walter)
DB (GGHPW).
GN
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Gallus.
OC NCBI_TaxID=9031;
RN SEQUENCE FROM N.A.
RN MEDLINE=94040816; PubMed=7901127;
RA Goldberg G.S.; Kaczmarczyk W.;
RT "A chicken genomic DNA fragment that hybridizes to the murine Hox-3.1
RT homeobox is likely to encode the NADH ubiquinone oxidoreductase
RT subunit B15." (By similarity).
RN PRT
RN SEQUENCE FROM N.A.
RN MEDLINE=93077061; PubMed=1359990;
RA Goldberg G.S.; Kaczmarczyk W.;
RT "Sequence of a novel chicken genomic DNA fragment that hybridizes to
RT the murine Hox-3.1 homeobox.";
RL Gene 121:397-398(1992).
CC - FUNCTION: TRANSFER OF ELECTRONS FROM NADH TO THE RESPIRATORY
CC CHAIN. THE IMMEDIATE ELECTRON ACCEPTOR FOR THE ENZYME IS BELIEVED
CC TO BE UBIQUINONE (BY SIMILARITY).
CC - CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
CC - CATALYTIC ACTIVITY: NADH + acceptor = NAD(+) + reduced acceptor.
CC - SUBUNIT: COMPLEX I IS COMPOSED OF ABOUT 40 DIFFERENT SUBUNITS.
CC - SUBCELLULAR LOCATION: Mitochondrial inner membrane; matrix side
CC (By similarity).

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OM protein - protein search, using sw model

Run on: January 29, 2004, 09:09:06 ; Search time 35 Seconds

Perfect score: 678 (without alignments)

Title: US-09-726-899-3
Sequence: 1 MSFPKYKPPSSLRLTPETLDP.....DRKEKLIQEGKLDRTFHLSY 129

Scoring table: BL0SUM62 Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL 23 :*

1: sp_archea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rabbit:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacteriaph:*

17: sp_archeap:*

Q8v3f4 swinepox vi

Q8gtcz2 oryza sativ

Q91wf40 mus musculu

Q91wf11 arabidopsis

Q91g30 arabidopsis

Q9fkf2 arabidopsis

Q8i4u7 plasmoidium

Q9u3ub plasmoidium

Q94mz5 haemophilus

Q8ikz6 plasmoidium

Q9xf46 phaseolus a

Q9xf13 phaseolus v

Q92xv2 rhizobium m

Q9zb47 streptococc

Q9i8d1 gallus galli

Q8biy3 mus musculu

Q8iwl0 homo sapien

Q9v1j3 drosophila

Q8ln91 oryza sativ

Q8s8i1 arabidopsis

Q8bwj9 homo sapien

Q8nai1 homo sapien

Q8tu41 methanoscarc

Q93w10 oryza sativ

Q9y2z0 homo sapien

Q9d9b7 mus musculu

ALIGNMENTS

RESULT	1	Q8N4D3	PRELIMINARY;	PRT;	119 AA.
ID	Q8N4D3				
AC	Q8N4D3;				
DT	01-OCT-2002 (Tremblrel. 22, Created)				
DR	01-OCT-2002 (Tremblrel. 22, Last sequence update)				
KW	Hypothetical protein (Fragment).				
OS	Hom sapiens (Human)				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX					
NCBI_TaxID	9606;				
[1]					
RN	SEQUENCE FROM N.A.				
RC	TISUB-Brain;				
RA	Strasbourg R.;				
RL	Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; BC034579; AAH34579.1; -.				
KW	Hypothetical protein.				
FT	NON_TER	1			
SQ	SEQUENCE	119 AA;	13921 MW;	38EAPA4685AED9BA CRC64;	

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARS

Result No.	Query	Match	Length	DB ID	Description
1	569	83.9	119	4 Q8N4D3	Q8n4d3 homo sapien
2	529	78.0	129	11 Q9CQC7	Q9cqg7 mus musculu
3	236	34.8	119	11 Q9DBH2	Q9abh2 mus musculu
4	115.5	17.0	172	5 Q23098	Q23098 caenorhabdi
5	96.5	14.2	113	5 Q9V753	Q9v753 drosophila
6	82	12.1	386	2 Q9L7P6	Q9l7p6 yersinia pe
7	82	12.1	757	16 Q8ZI43	Q8zi43 yersinia pe
8	78	11.5	764	17 Q8TZH8	Q8tzh8 pyrococcus
9	75.5	11.1	980	16 Q9B2K5	Q9b2k5 rhabdophila
10	74.5	11.0	313	2 Q9KI98	Q9ki98 bacteroides
11	74	10.9	173	16 Q8FVM0	Q8fvm0 corynebacte
12	74	10.9	195	11 Q9WUN8	Q9wun8 mus musculu
13	74	10.9	308	16 Q9HW70	Q9hw70 pseudomonas
14	74	10.9	526	2 Q9WXH9	Q9wxh9 lactobacill
15	73	10.8	199	16 Q8D1Z8	Q8d1z8 synechococc
16	73	10.8	634	13 Q9OY16	Q9oy16 fugu rubrip

RESULT	2	Q9CQC7	PRELIMINARY;	PRT;	129 AA.
ID	Q9CQC7				
AC	Q9CQC7;				
DT	01-OCT-2002 (Tremblrel. 22, Last annotation update)				
DR	01-OCT-2002 (Tremblrel. 22, Last annotation update)				
KW					
FT					
SQ	SEQUENCE	119 AA;	13921 MW;	38EAPA4685AED9BA CRC64;	

Query	2 SFPKXPKSSLRLTPETLDPAYNISPETRRAQERLAIHQKREYLQYNDPNNRGLIE 61	Score	83.9%	Score	569;
Best Local Similarity	100.0%	Pred. No.	3.5e-54;	DB 4;	Length 119;
Matches	108;	Conservative	0;	Mismatches	0;
Indels	0;	Gaps	0;		
Query	2 SFPKXPKSSLRLTPETLDPAYNISPETRRAQERLAIHQKREYLQYNDPNNRGLIE 60	Score	83.9%	Score	569;
Best Local Similarity	100.0%	Pred. No.	3.5e-54;	DB 4;	Length 119;
Matches	108;	Conservative	0;	Mismatches	0;
Indels	0;	Gaps	0;		
Query	2 SFPKXPKSSLRLTPETLDPAYNISPETRRAQERLAIHQKREYLQYNDPNNRGLIE 61	Score	83.9%	Score	569;
Best Local Similarity	100.0%	Pred. No.	3.5e-54;	DB 4;	Length 119;
Matches	108;	Conservative	0;	Mismatches	0;
Indels	0;	Gaps	0;		
Query	2 SFPKXPKSSLRLTPETLDPAYNISPETRRAQERLAIHQKREYLQYNDPNNRGLIE 60	Score	83.9%	Score	569;
Best Local Similarity	100.0%	Pred. No.	3.5e-54;	DB 4;	Length 119;
Matches	108;	Conservative	0;	Mismatches	0;
Indels	0;	Gaps	0;		
Query	2 SFPKXPKSSLRLTPETLDPAYNISPETRRAQERLAIHQKREYLQYNDPNNRGLIE 61	Score	83.9%	Score	569;
Best Local Similarity	100.0%	Pred. No.	3.5e-54;	DB 4;	Length 119;
Matches	108;	Conservative	0;	Mismatches	0;
Indels	0;	Gaps	0;		
Query	2 SFPKXPKSSLRLTPETLDPAYNISPETRRAQERLAIHQKREYLQYNDPNNRGLIE 60	Score	83.9%	Score	569;
Best Local Similarity	100.0%	Pred. No.	3.5e-54;	DB 4;	Length 119;
Matches	108;	Conservative	0;	Mismatches	0;
Indels	0;	Gaps	0;		

DT	01-JUN-2001 (TREMBLrel. 17, Created)		
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)		
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)		
DE	0610006N12RIK protein.		
EN	0610006N12RIK.		
EN	Mus musculus (Mouse).		
DC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
DX	NCBI_TaxID=10090;		
DN	[1]		
RP	SEQUENCE FROM N.A.		
RP	STRAIN=C57BL/6J; TISSUE=Kidney, and Tongue; MEDLINE=221085660; PubMed=11217851;		
RX	Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Harada A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Iwasa M., Nishi K., Kiyosawa H., Kondo S., Yamamoto I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Saito K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Flieischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis P., Matsuo Y., Nikaido I., Pebole G., Quackenbush J., Sakai K., Okido T., Furuno M., Aono H., Balldarelli R., Barsh G., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Schoenbach C., Sato K., Schoenbach C., Suya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Hayashizaki Y., "Functional annotation of a full-length mouse cDNA collection.";		
RX	Query Match : 78 0%; Score 529; DB 11; Length 129; Best Local Similarity 75.2%; Pred. No. 8.8e-50; Matches 97; Conservative 16; Mismatches 0; Gaps 0;		
RX	SEQUENCE : 129 AA; 15081 MW; 9E7B85087F095062 CRC64;		
RP	SEQUENCE FROM N.A.		
RP	STRAIN=C57BL/6J; TISSUE=Liver; MEDLINE=22085660; PubMed=11217851;		
RX	Kawai J., Shinsagawa A., Metzoya T., Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
RX	NCBI_TaxID=10090;		
RX	[1]		
RP	SEQUENCE FROM N.A.		
RP	STRAIN=C57BL/6J; TISSUE=Liver; MEDLINE=22085660; PubMed=11217851;		
RX	Kawai J., Shinsagawa A., Shibusawa K., Yoshino M., Itoh M., Ishii Y.,		

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OM protein - protein search, using sw model

Run on: January 29, 2004, 08:58:40 ; Search time 42 Seconds
 (without alignments)
 487.517 Million cell updates/sec

Title: US-09-726-899-3
 Perfect score: 678
 Sequence: 1 MSFPKXKPSSLRLPDTLDP.....DRKEKLIQEGKLDRTFHLSY 129

Scoring table: BL0SUM62
 Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : A_Geneseq19Jund03 : *
 1 : /SIDSL1/gcdata/geneseq/geneseq-emb1/AA1980.DAT : *
 2 : /SIDSL1/gcdata/geneseq/geneseq-emb1/AA1181.DAT : *
 3 : /SIDSL1/gcdata/geneseq/geneseq-emb1/AA1982.DAT : *
 4 : /SIDSL1/gcdata/geneseq/geneseq-emb1/AA1983.DAT : *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STATEMENT

8667-ΠΟΩ-Σ7

17-DBSC-1997: 97

1 / AN-193 / 3 / 03-0 / 83083

TNU-1 TNU-2

- 1 -

Bandman O., Goli

Novel human secret	AAU33022	AAU33023	ABG22982	AGT13633	ABR16749
Novel human diagno					
Novel human colon cance					
Drosophila melanoc					

ATTEMPTS

Human bone marrow	10	1.1	155	2.2	ABB12358
Recombinant P. fur	11	11.5	764	2.2	AAB62028
Human colon cancer	11	11.2	16	2.1	AAB53504
Putative P. abyssi	12	11.2	451	2.2	AAB96180
Novel human diagno	13	10.9	1746	2.2	ABG05869
Zea mays protein f	13	10.9	72	2.0	ABG05869
Candida albicans e	14	10.7	72	2.0	ABG05869
Human nucleic acid	14	10.7	72	2.0	ABG05869
Plasmodium falciparum	15	10.6	72	2.0	ABG05869
Human polypeptide	15	10.6	72	2.0	ABG05869
Protein involved i	15	10.6	72	2.0	ABG05869
Orzyza sativa Cdc6	16	10.4	936	2.3	ABP13605
Human methylene-te	17	10.3	432	2.3	ABG05869
Human methylene-te	18	10.3	1025	2.3	ABP52133
Human methylene-te	19	10.3	120	2.2	AA001882
Human methylene-te	19	10.3	292	2.1	AA055797
Human methylene-te	20	10.3	294	2.0	AAW05690
Human methylene-te	21	10.3	656	1.7	AAR08358
Human methylene-te	22	10.2	656	2.2	AAE12607
Human methylene-te	23	10.2	656	2.2	AAE12607
Human methylene-te	24	10.2	656	2.3	AAO15894
Human methylene-te	25	10.2	660	1.7	AAR08359
Human methylene-te	26	10.2	660	2.1	AAV06186
Human methylene-te	27	10.2	660	2.2	AAE12606
Human methylene-te	28	10.2	660	2.3	AAU75413
Human methylene-te	29	10.2	660	2.3	AAU75421
Human methylene-te	30	10.2	660	2.3	AAU75422
Human methylene-te	31	10.2	660	2.3	AAU75424
Human methylene-te	32	10.2	660	2.3	AAU75425
Human methylene-te	33	10.2	660	2.3	AAU75426
Human methylene-te	34	10.2	660	2.3	AAU75428
Human methylene-te	35	10.2	660	2.3	AAU75429
Human methylene-te	36	10.2	660	2.3	AAU75430
Human polypeptide,	37	10.2	760	2.2	AAW0803
Human interferon-a	38	10.2	760	2.2	AAW0803
Drosophila melanog	39	10.2	1026	2.2	ABE04339
Arabidopsis thalia	40	10.1	204	2.1	AAG54044
Arabidopsis thalia	41	10.1	237	2.1	AAG54045
Arabidopsis thalia	42	10.1	42	2.1	AAG54043
Arabidopsis thali	43	10.1	294	2.1	AAG54044
Arabidopsis thali	44	10.1	294	2.1	AAG54045
Arabidopsis thali	45	10.1	350	2.1	AAG54045

RESULT 1
 AAW69225
 ID AAW69225 standard; Protein: 129 AA.
 XX
 AC
 AAW69225;
 XX
 XX
 DE NADH dehydrogenase subunit NDS-2.
 DE NADH dehydrogenase subunit; sympathetic nervous system disease; myo-
 nicotinamide-adenine dinucleotide dehydrogenase; cancer; leukaemia; NDS-2
 KW immune system disease; disorder; nervous system disease; Tharavani; NDS-2
 KW

Homo sapiens.
WO9831815-A2.
23-JUL-1998.
17-DBC-1997; 97WO-US23970.
17-JAN-1997; 97US-0785065.
(INCYT-) INCYTE PHARM INC.
Bandman O, Goli SK, Hillman JL;
WPI; 1998-414112/35.
N-PSDB; AAV44787.
Human nicotinamide-adenine dinucleotide dehydrogenase sub:units

useful for, e.g. diagnosis, treatment and prevention of cancer, myopathy, immune system disease and neurodegeneration.

Claim 19; Fig 2; 80pp; English.

This sequence represents the NADH (reduced nicotinamide-adenine dinucleotide) dehydrogenase subunit, NDS-2, of the invention. Cells containing the DNA are used to produce the recombinant subunits. Antagonists of NDS-1 (typically antisense sequences or ribozymes) are used to treat or prevent cancer (leukaemia and solid cancers) and immune system disorders (e.g. asthma, diabetes, rheumatoid arthritis, osteoporosis and many others); NDS-2 and NDS-4 are used to treat myopathy (e.g. ophthalmoplegia, myoclonic epilepsy and lactic acidosis) while their antagonists are used to treat cancer and disease of the sympathetic nervous system (e.g. hypertension, arrhythmia and migraine); NDS-3 is also used to treat myopathy and its antagonists to treat cancer and neurodegenerative disease (e.g. Alzheimer's, Huntington's and Parkinson's diseases, epilepsy and Down's syndrome). In all cases NDS or their antagonists may be expressed from gene therapy vectors. Ab may be used therapeutically as antagonist as immunoassay reagent for agents that monitoring such diseases; in competitive screening assays for agents that bind specifically to the subunits, and for affinity purification of the subunits from natural sources. The DNAs are useful as primers and probes for diagnosis and monitoring (including detecting predisposition to cancer); for gene mapping or identifying related sequences, while the subunits are also used to raise antibodies and to screen for specific binding agents.

Sequence	129 AA:	Query	Match	100.0%	Score	678;	DB	19;	Length	129;
		Best Local Similarity	100.0%	Pred. No.	2.1e-13;					
		Matches 129;	Conservative Matches	0;	Mismatches	0;	Indels	0;	Gaps	0;
		1	MSFPKYPKSSRLTLPELDPAYNISPESTRRAQAERLAIRAQKREYLLQYNDENRGRHLI	60						
		1	MSFPKYPKSSRLTLPELDPAYNISPESTRRAQAERLAIRAQKREYLLQYNDENRGRHLI	60						
		61	ENPALLRWAVARTINTVNPFRTPPKQSLMGALCGPGLPIFIYIYIKTERDRKEKLIDQEK	120						
		61	ENPALLRWAVARTINTVNPFRTPPKQSLMGALCGPGLPIFIYIYIKTERDRKEKLIDQEK	120						
		121	LDRTEPHLSY	129						
		121	LDRTEPHLSY	129						

RESULT: 2
ID: B12440 Standard; Protein: 294 AA.
AC: ABB12440;
DT: 15-JAN-2002 (first entry)
DE: Human bone marrow expressed protein SEQ ID NO: 279.
KW: Human; bone marrow; cytostatic; antiarthritic; vulnerability;
antiinflammatory; antibacterial; immunosuppressive; vasotrophic; cancer;
anticarboxypeptidase; neuroprotective; nootropic; haemostatic; osteopathic;
antiulcer; fungicide; antidiabetic; antiasthmatic; antiallergic;
immunostimulant; analgesic; cerebroprotective; antihaemocytic; infection;
nervous system disorder; autoimmune disorder; inflammation; allergy.
CC: Homo sapiens.
DB: WO200174836-A1.
DA: 11-OCT-2001.
DR: 30-MAR-2001; 2001WO-US10472.
DR: 31-MAR-2000; 2000US-0540217.

PR 23-AUG-2000; 2000US-0649167.
PR 23-AUG-2000; 2000US-0649267.
PR 30-NOV-2000; 2000US-2505839.P.
XX (HYSEB-) HYSEQ INC.
XX PI Tang YT, Liu C, Drmanac RT
XX DR WPI: 2001-626375/72.
XX PT New bone marrow-expressed nu-
diagnosis, treatment of infl-
and increasing hematopoiesis
remodeling -
XX PT
XX PS Claim 10; Page 331; 380pp; E
XX CC The present invention relates
CC and proteins. These sequences
CC inflammatory conditions (eg
CC and peripheral nervous system
CC Alzheimer's, Parkinson's and
CC disorders, head trauma, cere-
CC cell disorders, platelet dis-
CC degenerative disorders, auto-
CC sclerosis, diabetes and arth-
CC allergies and blood coagulat-
CC protein of the invention.

XX	Sequence	294 AA;	Score	530;	DB	22;	Length	294;
SQ		Query Match	78.2%;		Pred.	No.	4.1e-55;	
		Best Local Similarity	84.6%;					
		Matches	104;	9;	Mismatches	8;	Indels	2;
		Conservative					Gaps	2;
QY	1	MSFPKYPKSSLRTLPTLDPAEYNISSETRAAERLAIRQLKREYLLQYNDPQRGLI	60					
Db	80	MSFPKYPKSSLRTLPTLDPAEYNISSETRAAERLAIRQLKREYLLQYNDPQRGLI	139					
QY	61	ENPALLIRWARTINVPNFKPTPKSSLMGA-LCGFGLIPIFYIYIKTER-DREKELIQE	118					
Db	140	ENPALLIRWARTINVPNFKPTPKSSLMGA-FWDGPLIPIFYIYIKTERWDPNQRWLTD	199					
QY	119	GKL 121						...

KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.
 XX
 OS Homo sapiens.
 XX
 PN WO200179449-A2.
 XX
 PD 25-OCT-2001.
 XX
 PP 16-APR-2001; 2001WO-US08656.
 XX
 PR 18-APR-2000; 2000US-0552929.
 PR 26-JAN-2001; 2001US-0770160.
 (HYSEQ) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Drmanac RT;
 XX
 PA (HYSEQ) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Drmanac RT;
 XX
 DR 2001-611725/70.
 XX
 PT Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy -
 XX
 PS Claim 20; Page 699; 765pp; English.
 XX
 PT Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy -
 XX
 PS Claim 20; Page 699; 765pp; English.
 XX
 The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising the nucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and therapy, and can be used as nutritional supplements. They may be used to increase stem cell proliferation; to regulate haemopoiesis; and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or stimulation; as anti-inflammatory agents; and in treatment of leukaemias. AAU29510-AAU3304 represent the amino acid sequences of novel human secreted proteins of the invention.
 XX
 Sequence 119 AA;
 Query Match 69.8%; Score 473; DB 22; Length 119;
 Best Local Similarity 73.9%; Prod. No. 8.9e-49;
 Matches 88; Conservative 14; Mismatches 17; Indels 0; Gaps 0;
 SQ
 Query 5 KYKPPSSLRTLPEPLDPAYNISPETRQQAERLIAKREYLQYNDPNERGLTENPA 64
 1 KTYLSSLRATVPPPLNPAYNISDTRRAQEQLAIRGLKXYLLQYNPNERGLTIDPA 60
 DB 65 LIRWYATINTVNPFRTPKRSIPLGALGFGPLIFTYIITTERDRKEKLQEGKDR 123
 61 LIRWTYAATSYNPFRTPKRSIPLGALCAFGPLFWYCVFRMDRKTETLPEGKLUQ 119
 RESULT 6
 AAU33023 standard; Protein: 115 AA.
 XX
 ID AAU33023 (first entry)
 XX
 DE Novel human secreted protein #3514.
 XX
 KW Human; vaccination; gene therapy; nutritional supplement;
 KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;
 KW immune suppression; immune stimulation; anti-inflammatory;
 OS Homo sapiens.

KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.
 XX
 OS WO200179449-A2.
 XX
 PN 25-OCT-2001.
 XX
 PP 16-APR-2001; 2001WO-US08656.
 XX
 PR 18-APR-2000; 2000US-0552929.
 PR 26-JAN-2001; 2001US-0770160.
 (HYSEQ) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Drmanac RT;
 XX
 PA (HYSEQ) HYSEQ INC.
 XX
 PT Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy -
 XX
 PS Claim 20; Page 699; 765pp; English.
 XX
 The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising the nucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and therapy, and can be used as nutritional supplements. They may be used to increase stem cell proliferation; to regulate haemopoiesis; and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or stimulation; as anti-inflammatory agents; and in treatment of leukaemias. AAU29510-AAU3304 represent the amino acid sequences of novel human secreted proteins of the invention.
 XX
 Sequence 115 AA;
 Query Match 60.2%; Score 408; DB 22; Length 115;
 Best Local Similarity 66.1%; Prod. No. 5.6e-41;
 Matches 76; Conservative 16; Mismatches 23; Indels 0; Gaps 0;
 SQ
 Query 9 SSPLRTPPLDPAYNISPETRQQAERLIAKREYLQYNDPNERGLTENPA 68
 1 SSLLATPANLNPEYSISPDNRRAQEQLAIRGLKXYLLQYNPNERGLTIDPA 60
 DB 69 AYARTINTVNPFRTPKRSIPLGALGFGPLIFTYIITTERDRKEKLQEGKDR 123
 61 TYARSANVNPFRTPKRSIPLGALCAFGPLFWYCVFRMDRKTETLPEGKLUQ 115
 RESULT 7
 ABG22982 standard; Protein: 68 AA.
 ID ABG22982;
 XX
 AC ABG22982;
 XX
 DT 18-FEB-2002 (first entry)
 XX
 DB Novel human diagnostic protein #22973.
 XX
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200175067-A2.
 XX
 PD 11-OCT-2001.
 XX
 PP 30-MAR-2001; 2001WO-US08631.

XX PR 31-MAR-2000; 2000US-0540217.
 XX PR 23-AUG-2000; 2000US-0649167.
 XX (HYSE-B) HYSEQ INC.
 XX PA Drmanac RT, Liu C, Tang YR;
 XX DR WPI; 2001-639362/73.
 XX N-PSDB; AASB7169.
 XX New isolated polynucleotide and encoded polypeptides, useful in PT diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess PT biodiversity -
 XX PT Claim 20; SEQ ID No 53341; 103pp; English.
 PS The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG0010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at [ftp.wipo.int/pub/published_pct_sequences](http://wipo.int/pub/published_pct_sequences).
 XX SQ Sequence 68 AA;
 CC Query Match 39 4%; Score 267; DB 22; Length 68;
 CC Best Local Similarity 100.0%; Pred. No. 2.7e-24;
 CC Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC RESULT 9
 CC ID AAG73633 standard; Protein; 33 AA.
 CC DB 9 ENPALLRWARTINYNPRTPKNSLGAALCGFGPLFIVVYIKTER 109
 CC AC AAG73633;
 CC DT 03-SEP-2001 (first entry)
 CC DE Human colon cancer antigen protein SEQ ID NO:4397.
 CC KW Human; colon cancer; colon cancer antigen; diagnosis; detection; colorectal carcinoma.
 CC OS Homo sapiens.
 CC PN WO200122920-A2.
 CC PD 05-APR-2001.
 CC XX 28-SEP-2000; 2000WO-US26524.
 CC XX 29-SEP-1999; 99US-0157137.
 PR 03-NOV-1999; 99US-0163280.
 XX PA (HUNA-) HUMAN GENOME SCI INC.
 XX PI Ruben SM, Barash SC, Birse CB, Rosen CA;
 XX DR WPI; 2001-235157/24.
 DR N-PSDB; AAH33064.
 XX PR Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers -
 XX PS Claim 11; Page 6222-6223; 9803pp; English.
 XX AAH2943 to AAH37195 and AAH373514 to AAH7788 represent human colon cancer-associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P expression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing inactive proteins or to supplement the patient's own production of P. Additionally, N may be used to produce the colon cancer-associated P, by inserting the nucleic acids into a host cell and culturing the cell to express the proteins. N and P can be used in the prevention, diagnosis and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204 and AAB7789 represent sequences used in the exemplification of the present invention.
 CC N B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present for CC SEQ ID NO:1027 to 1052, 7921 and 7922.
 XX SQ Sequence 33 AA;
 CC Query Match 18.3%; Score 124; DB 22; Length 33;
 CC Best Local Similarity 100.0%; Pred. No. 1.7e-07;
 CC Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC AC ABB67497;
 CC YY 106 KTERRKERKLIQEGKLDRTPHLY 129
 CC XX 10 KTERRKERKLIQEGKLDRTPHLY 33
 CC DB 106 KTERRKERKLIQEGKLDRTPHLY 129
 CC XX 10 KTERRKERKLIQEGKLDRTPHLY 33
 CC AC ABB67497;
 CC XX 26-MAR-2002 (first entry)
 CC DE Drosophila melanogaster polypeptide SEQ ID NO 29283.
 CC KW Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.
 CC OS Drosophila melanogaster.
 CC PN WO200171042-A2.
 CC PD 27-SEP-2001.
 CC XX 23-MAR-2001; 2001WO-US0231.
 CC PP (PEKE) PE CORP NY.
 CC XX 23-MAR-2000; 2000US-191637P.
 CC PR 11-JUL-2000; 2000US-0614150.
 CC PA (PEKE) PE CORP NY.
 CC XX 28-SEP-2000; 2000WO-US26524.
 CC PI Venter JC, Adams M, Li PWD, Myers EW;

DR WPI; 2001-656860/75.
 DR N-PSDB; ABL1600.
 PT New isolated nucleic acid detection reagent for detecting 1000 or more genes from *Drosophila* and for elucidating cell signalling and cell-cell interactions -
 XX Disclosure, SEQ ID NO 29283; 21pp + Sequence Listing; English.
 XX The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from *Drosophila*. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (AB16176-AB13051), expressed DNA sequences (AB101840-AB116175) and the encoded proteins (AB57737-AB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 XX Sequence 113 AA;
 SQ Query Match 14.2%; Score 96.5; DB 22; Length 113;
 Best Local Similarity 29.3%; Pred. No. 0.0018;
 Matches 27; Conservative 20; Mismatches 36; Indels 9; Gaps 3;
 XX 42 QLKREYLLQYNDPNNR----GLIENPALLRWAYARTTINYVNPFRPTPKNSLMLGALCGFG 96
 QY 20 KLRQEFKQSNPQYHATGEGTTFDAGLARFOAMRVSN-YEHFKPTGKSRTGFLFAVVL 78
 Db 97 PLIPIYIILKTERDRKEKLIGBKL---DRTF 125
 QY 79 PIALYAWALKAERDGRGEKREKYTGQVAYKDROF 110
 Db

RESULT 10
 ABB12358
 ID ABB12358 standard; Protein; 155 AA.
 XX AC ABB12358;
 XX DT 15-JAN-2002 (first entry)
 XX DE Human bone marrow expressed protein SEQ ID NO: 112.
 XX Human; bone marrow; cytostatic; antirheumatic; antiarthritic; vulnerary; antiinflammatory; antibacterial; immunosuppressive; vasotropics; cancer; antiparkinsonian; neuroprotective; notropic; haemostatic; osteopathic; antiallergic; fungicide; antidiabetic; antiasthmatic; antiallergic; immunostimulant; analgesic; cerebroprotective; antianæmic; infection; nervous system disorder; autoimmune disorder; inflammation; allergy.
 XX OS Homo sapiens.
 PN WO200174836-A1.
 XX PD 11-OCT-2001.
 XX PF 30-MAR-2001; 2001IWO-US104727.
 XX PR 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0549167.
 PR 23-AUG-2000; 2000US-0649267.
 PR 30-NOV-2000; 2000US-250583P.
 XX PA (HYSEQ) HYSEQ INC.
 PT Tang YT, Liu C, Drmanac RT, Ford JE, Boyle BJ;
 XX PS Claim 182; Fig 32; 147pp; English.
 DR N-PSDB; ABA09602.
 XX DR N-PSDB; ABA09602/72.
 XX CC The invention provides a composition (A) for enhancing nucleic acid polymerase reactions that comprises an archaeal MCM (minichromosome

PT New bone marrow-expressed nucleic acids and polypeptides, useful for diagnosis, treatment of inflammatory, autoimmune, neurological, cancer and increasing hematopoiesis, stem cell survival and bone growth and remodeling -
 XX Claim 10; Page 221; 380pp; English.
 PS XX The present invention relates to bone marrow expressed polynucleotides and proteins. These sequences can be used in the treatment of inflammatory conditions (eg arthritis, Crohn's disease), cancer, central and peripheral nervous system diseases and neuropathies, such as Alzheimer's, Parkinson's and Huntington's diseases, spinal cord disorders, head trauma, cerebrovascular diseases, myeloid and lymphoid cell disorders, platelet disorders, stem cell disorders, bone degenerative disorders, autoimmune disorders, for example multiple sclerosis, diabetes and bacterial infections, viral and bacterial infections, allergies and blood coagulation disorders. The present sequence is a protein of the invention.
 XX Sequence 155 AA;
 SQ Query Match 14.1%; Score 95.5; DB 22; Length 155;
 Best Local Similarity 32.7%; Pred. No. 0.0036;
 Matches 34; Conservative 6; Mismatches 27; Indels 37; Gaps 5;
 XX Qy 1 MSFPKYP-----SISRTLPTLDPAEYNISPTERRQAERLAIARAQKRE-YLQYNDP 54
 Db 80 MSFPKYPCEPAHSAYR--PSTQPNPTYLRKGGRK--PERIAHRSPAANESTLQYNDP 135
 Qy 55 NRGGLLENPALLRWAYARTTINYVNPFRPTPKNSLMLGALCGFGPL 98
 Db 136 N-----TPEAHRKSVPCFVGPML 152

RESULT 11
 AAB62028
 ID AAB62028 standard; Protein; 764 AA.
 XX AC AAB62028;
 XX DT 14-MAY-2001 (first entry)
 XX DB Recombinant P. furiosus helicase 5.
 XX MC MCM; minichromosome maintenance protein; archaeal polypeptide; PCNA;
 KW RFC-P28; RFC-P55; RPA; CDC6; FEN-1; dUTPase; helicase dna2; PCR;
 KW helicase 5; nucleic acid amplification; polymerase chain reaction.
 XX OS Pyrococcus furiosus.
 XX PN WO200109347-A2.
 XX PD 08-FEB-2001.
 XX PP 28-JUL-2000; 2000WO-US20532.
 XX PR 30-JUL-1999; 99US-0146580.
 XX PA (STRA-) STRATAGENE.
 XX PI Hogrefe HH, Cline JM, Hansen CJ, Borns MC;
 XX DR WPI; 2001-182959/18.
 DR N-PSDB; AAF7032.
 XX PT Composition for improving nucleic acid polymerase reactions, useful e.g. in synthesis or amplification, contains at least one archaeal
 PT accessory protein -
 XX PS Claim 182; Fig 32; 147pp; English.
 XX CC The invention provides a composition (A) for enhancing nucleic acid polymerase reactions that comprises an archaeal MCM (minichromosome

CC maintenance protein) and at least one of the archaeal polypeptides (PCNA, CC RPF-P38 or -P55, RPA, CDC6, FEN-1, dUTPase, ligase, helicase dna, or CC helicases 2-8). (A) And similar compositions containing different CC synthetics, amplification, mutagenizing, labeling and detecting reactions, CC e.g. for gene characterization, cloning, detection of allelic variants, CC diagnosis and screening for disease, particularly where done by CC polymerase chain reaction (PCR). Some of the proteins also stabilize CC duplexes during polymerase reactions or improve exonuclease reactions, CC for example RPA also improves specificity of nucleic acid/protein CC interaction and PCNA improves polymerase-mediated repair processes and CC hybridization reactions. Nucleic acids encoding the archaeal polypeptides CC are used for recombinant production of proteins, and fragments of the CC nucleic acid as probes and primers for screening, related sequences. The CC accessory proteins increase accuracy and efficiency of polymerase CC reactions, allow use of lower denaturation and extension temperatures CC (possibly isothermal processing), and improve synthesis of long targets. CC The present sequence represents a *P. furiosus* recombinant helicase 5. XX

Sequence 764 AA;

Query Match 11.5%; Score 78; DB 22; Length 764;
 Best Local Similarity 25.8%; Pred. No. 3.8;
 Matches 33; Conservative 21; Mismatches 30; Indels 44; Gaps 7;
 SQ

Qy	16	ETLDPEAYNISPETRAAQAEELAIAQQLREYLQQNNDPNERGLIENPALLRWARTI-	74
Db	578	KTLDVGDYIIS-----EDVAIERSKANDFIQSIIDGR--LFHQVRLIKEATSRPIM	626
Qy	75	-----NVYPNFRPTPKNSLMGACG---FG-PLIF-----IYIYIKTER 109	
Db	627	IVEGSLYIGTRNVP-----NAIRGAAIAAVTVDFGVPIIFSSTPBPETAQVFLIAKREQ	679
Qy	110	DRKEKLIQ 117	
Db	680	EREREKPV 687	

RESULT 12

AAB53504 ID AAB53504 standard; Protein; 16 AA.
 XX AC AAB53504;
 XX DT 09-MAR-2001 (first entry)

XX Human colon cancer antigen protein sequence SEQ ID NO:1044.
 XX KW Human; colon cancer; colon cancer antigen; diagnosis; detection;
 KW identification; cytosatic; cardioactive; neuroprotective; pulmonary;
 KW immunomodulatory; muscular; gynaecological; gastrointestinal;
 KW nephrotropic; antiinfective; antibacterial; gene therapy; wound;
 KW neural disorder; immune system disorder; muscular disorder;
 KW reproductive disorder; gastrointestinal disorder; renal disorder;
 KW infectious disease; cardiovascular disorder.
 XX OS Homo sapiens.
 XX WO200055151-A1.
 XX PN 21-SEP-2000.
 XX PD 08-MAR-1999; 99US-0124270.
 XX PA (HUMA-) HUMAN GENOME SCI INC.
 XX PI Rosen CA, Ruben SM;
 XX PR 12-MAR-1999; 99US-0124270.
 XX PA (HUMA-) HUMAN GENOME SCI INC.

XX WO200055151-A1.
 XX PN 21-SEP-2000.
 XX PD 08-MAR-1999; 99US-0124270.
 XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Forterre P, Thierry JC, Prieur D, Dietrich J, Lecompte O;
 XX PI Querellou J, Weissenbach J, Saurin W, Heilig R,
 XX DR WPI; 2001-126236/14.
 XX PA (CNRS) CNRS CENT NAT RECH SCI.
 XX PA (IFRE) IFREMER INST FR RECH EXPL MER.
 XX PI Forterre P, Thierry JC, Prieur D, Dietrich J, Lecompte O;
 XX PI Querellou J, Weissenbach J, Saurin W, Heilig R,
 XX DR WPI; 2001-126236/14.
 XX PA (CNRS) CNRS CENT NAT RECH SCI.
 XX PA (IFRE) IFREMER INST FR RECH EXPL MER.

XX New nucleotide sequences isolated from *Pyrococcus abyssi* encode
 PT proteins useful in industry -
 XX PI Querellou J, Weissenbach J, Saurin W, Heilig R,
 XX DR WPI; 2001-126236/14.
 XX PA (CNRS) CNRS CENT NAT RECH SCI.
 XX PA (IFRE) IFREMER INST FR RECH EXPL MER.
 XX PI Forterre P, Thierry JC, Prieur D, Dietrich J, Lecompte O;
 XX PI Querellou J, Weissenbach J, Saurin W, Heilig R,
 XX DR WPI; 2001-126236/14.
 XX PA (CNRS) CNRS CENT NAT RECH SCI.
 XX PA (IFRE) IFREMER INST FR RECH EXPL MER.
 XX PI Forterre P, Thierry JC, Prieur D, Dietrich J, Lecompte O;
 XX PI Querellou J, Weissenbach J, Saurin W, Heilig R,
 XX DR WPI; 2001-126236/14.
 XX PA (CNRS) CNRS CENT NAT RECH SCI.
 XX PA (IFRE) IFREMER INST FR RECH EXPL MER.

CC The present invention relates to the genomic sequence of *Pyrococcus abyssi* CC abyssi (see AF86431 and AAH1223-7) and *P. abyssi* proteins. *P. abyssi* CC is isolated from deep-sea CC hydrothermal vents. The present sequence is one such *P. abyssi* protein.

PT Colon cancer associated gene sequences, referred to as colon cancer
 PT antigens, useful for the treatment, prevention, and diagnosis of colon
 PT disorders such as colon cancer -
 XX Claim 11; Page 1624; 2104pp; English.
 XX AAC97991 to AAC98763 encode the human colon cancer associated proteins,
 CC called human colon cancer antigens. Given in AAB53-34 to AAB54-06. The
 CC human colon cancer antigens can have cytosatic, cardioactive, muscular,
 CC neuroprotective, immunomodulatory, gynaecological, gastrointestinal,
 CC pulmonary, nephrotropic, antiinfective and antibacterial activities, and
 CC can be used in gene therapy. The colon cancer antigen polynucleotides,
 CC proteins and antibodies to the proteins are useful for the prevention,
 CC treatment and diagnosis of colon disorders, such as colon cancer. The
 CC polynucleotides may be used in diagnostics and research, such as for
 CC chromosome identification, and as hybridisation probes. The proteins
 CC may also be used to prevent diseases such as neural disorders, immune
 CC system disorders, muscular disorders, reproductive disorders,
 CC gastrointestinal disorders, wounds, renal disorders, infectious
 CC diseases, and cardiovascular disorders. AAC98764 to AAC98772 and
 CC AAB54007 represent sequences used in the exemplification of the present
 CC invention.
 XX Sequence 16 AA;
 SQ

Query Match	11.2%	Score 76;	DB 21;	Length 16;
Best Local Similarity	93.8%	Pred. No. 0.039;		
Matches	15;	Conservative 0;	Mismatches 1;	Indels 0;
Gaps	0;			

Qy 114 KLIQGKLDRTRFLHLSY 129
 Db 1 KLIQGKLDRTRFLHLSY 16

RESULT 13

AAB96680 ID AAB96680 standard; Protein; 451 AA.
 XX AC AAB96680;
 XX DT 29-OCT-2001 (first entry)
 XX DE Putative P. abyssi tryptophan synthase beta chain #1.
 XX KW Hyperthermophilic archaeon; hyperthermophilic protein.
 XX OS Pyrococcus abyssi.
 XX PN FR2792651-A1.
 XX PD 27-OCT-2000.
 XX PR 21-APR-1999; 99FR-0005034.
 XX PR 21-APR-1999; 99FR-0005034.
 XX DR WPI; 2001-126236/14.
 XX PA (CNRS) CNRS CENT NAT RECH SCI.
 XX PA (IFRE) IFREMER INST FR RECH EXPL MER.

The proteins of the present invention have various potential industrial uses, since the proteins are stable at very high temperatures, some up to 110 degrees centigrade.

Note: This patent is in the same patent family as WO2000065062, which contains additional sequences as shown in AAB99132-AAB99143, AAH75903-AAH75920 and AAK66436.

Sequence 451 AA;

Query Match 10.9%; Score 74; DB 22; Length 451;
 Best Local Similarity 32.6%; Pred. No. 5.8;
 Matches 29; Conservative 10; Mismatches 26; Indels 24; Gaps 5;
 Qy 11 LRTLPPLDPEYNISPET-----RRQAERLAIARQLKRYLQYNDPNRGLIE 61
 Db 29 LPDLFEPPLDPP--LDPETEPIDIEKLKRIFABEL-VKQEISRE---RY-----IE 73
 Qy 62 NPALLRWAYATINTVYNPFRTPKNSLMG 90
 Db 74 1PGBLKLYSKIGRPTPLFRATNLKLIG 102

RESULT 14

AABG05869 standard; Protein; 1746 AA.
 XX AABG05869;
 AC AAG33365;
 DT 13-FBB-2002 (first entry)
 XX Novel human diagnostic protein #5860.
 XX Human; chromosome mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX OS Homo sapiens.
 PN WO200175067-A2.
 XX 11-OCT-2001.
 XX 30-MAR-2001; 2001WO-US08631.
 XX (HYSE-) HYSEQ INC.
 PI Drmanac RT, Liu C, Tang YT;
 XX WPI: 2001-639362/73.
 DR N-PSDB; AAS70056

XX PR 23-AUG-2000; 2000US-0540217.

XX PR 23-AUG-2000; 2000US-0649157.
 PA (HYSE-) HYSEQ INC.
 PI Drmanac RT, Liu C, Tang YT;
 XX WPI: 2001-639362/73.

XX DR N-PSDB; AAS70056

XX PS 30-AUG-2000; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in

CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. AAB00010-AB03077 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this Patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at http://www.wipo.int/pdb/publiished_pct_sequences.

XX	Sequence	1746 AA;
Query	13 TLPELDPABYNISPETRAERLAIARQLKRYLQYNDPNRGLIE 61	Score 72.5; DB 22; Length 1746;
DB	1349 TLPSYYPPPTHSSKATRKLDPKREBEGNSKK---RFKOPDRNQLAGPYFRKAFPK 1404	Best Local Similarity 20.2%; Pred. No. 53; Mismatches 54; Indels 13; Gaps 2;
Qy	73 TINYVNPENFRTPKNSLMGALCGFGLIIFYIYIKTERDRKEKLIOEGKLG 121	Matches 22; Conservative 20; Mismatches 54; Indels 13; Gaps 2;
Db	1405 RLSFLNGLGFLGSLTTKAFPGVLPSSVSPYI-----TAMKBSVVGSQPI 1444	Qy 13 TLPELDPABYNISPETRAERLAIARQLKRYLQYNDPNRGLIE 61
XX	XX	DB 18-OCT-2000 (first entry)
XX	XX	DB Zea mays protein fragment SEQ ID NO: 40416.
XX	XX	XX Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; gene mapping; gene expression control; promoter; termination sequence; corn.
XX	XX	XX Zea mays subsp.. mayb.
XX	XX	XX PN EP1033405-A2.
XX	XX	XX PD 06-SEP-2000.
XX	XX	XX PR 25-FEB-2000; 2000EP-0301439.
XX	XX	XX PR 25-FEB-1999; 99US-0121825.
XX	XX	XX PR 05-MAR-1999; 99US-0123180.
XX	XX	XX PR 09-MAR-1999; 99US-0123548.
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XX	XX	XX PR 25-MAR-1999; 99US-0126264.
XX	XX	XX PR 29-MAR-1999; 99US-0126755.
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XX	XX	XX PR 16-APR-1999; 99US-0129845.
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PR	23-JUL-1999;	99US-0145224.	99US-0161044.
PR	26-JUL-1999;	99US-0145276.	99US-0161045.
PR	27-JUL-1999;	99US-0145913.	99US-0161406.
PR	27-JUL-1999;	99US-0145918.	99US-0161407.

PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161922.
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PR 29-OCT-1999; 99US-0162142.

Query Match Score 72; DB 21; Length 290;
Best Local Similarity 26.0%; Pred. No. 5.6;
Matches 32; Conservative 15; Mismatches 44; Indels 32; Gaps 6;
Matches 32; Conservative 15; Mismatches 44; Indels 32; Gaps 6;

Qy 4 PKYKPSSRLTLPETLDPAEYNISPETRAQERLAIRQLKREYLQYN--DPNRR--- 57
Db 10 PLFCPGPLVARE---PA---SSSPPPAGR PASOTLLARRAREKLDAMGYRKADPDLEAGGS 63

Qy 58 -----GLIENPALLRWAYARTINVNPNR----- 98
Db 64 SLLYPGTMTESPB-LRWAFLRKYVILTVQLMATAAVSAFVVKVPAVSNNPFSNAGIALY 122

Qy 99 IFI 101
Db 123 IFL 125

Search completed: January 29, 2004, 09:07:58
Job time : 43 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 29, 2004, 09:08:31 ; Search time 34 Seconds
(without alignments)

Title: US-09-726-899-3
Scoring table: BLASTM62
Perfect score: 678
Sequence: 1 MSPPKXPSSRLTLPETLDP.....DRKEKLIQEGKLDRTFHSY 129

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Published Applications AA: *

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB ID	Description
1	678	100.0	129	9 US-09-726-899-3	Sequence 3, Appli
2	522	77.0	117	12 US-09-726-899-10	Sequence 3428, Ap
3	514	75.8	129	9 US-09-726-899-10	Sequence 10, Appli
4	124	18.3	33	15 US-10-106-598-4407	Sequence 4407, Ap
5	76	11.2	16	11 US-09-925-299-1044	Sequence 1044, Ap
6	76	11.2	16	11 US-09-925-299-1044	Sequence 1044, Ap
7	71	10.5	433	12 US-10-369-93-21273	Sequence 21273, A
8	70.5	10.4	788	12 US-10-369-93-2648	Sequence 2648, Ap
9	70.5	10.4	936	12 US-10-03-585-744	Sequence 7442, Ap
10	70	10.3	337	10 US-09-014-777A-126	Sequence 126, Ap
11	70	10.3	340	10 US-09-814-777A-15	Sequence 15, Appli
12	70	10.3	384	10 US-09-814-777A-18	Sequence 18, Appli
13	70	10.3	384	10 US-09-814-777A-20	Sequence 20, Appli
14	70	10.3	470	10 US-09-814-777A-100	Sequence 100, Appli
15	70	10.3	680	12 US-10-369-93-3446	Sequence 3446, Ap

ALIGNMENTS

RESULT 1
US-09-726-899-3
; Sequence 3, Application US/097266899
; GENERAL INFORMATION:
; PATENT NO. US2001041356A1
; ATTORNEY/AGENT INFORMATION:
; APPLICANT: Baudman, Olga
; APPLICANT: Golli, Surya K.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: NOVEL SUBUNITS OF NADH DEHYDROGENASE
; NUMBER OF SEQUENCES: 112
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 31174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/726, 899
; FILING DATE:
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/785, 065
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36, 749
; REFERENCE/DOCKET NUMBER: PF-0187 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	678	100.0	129	9 US-09-726-899-3	Sequence 3, Appli
2	522	77.0	117	12 US-09-264-049-3428	Sequence 3428, Ap
3	514	75.8	129	9 US-09-726-899-10	Sequence 10, Appli
4	124	18.3	33	15 US-10-106-598-4407	Sequence 4407, Ap
5	76	11.2	16	11 US-09-925-299-1044	Sequence 1044, Ap
6	76	11.2	16	11 US-09-925-299-1044	Sequence 1044, Ap
7	71	10.5	433	12 US-10-369-93-21273	Sequence 21273, A
8	70.5	10.4	788	12 US-10-369-93-2648	Sequence 2648, Ap
9	70.5	10.4	936	12 US-10-03-585-744	Sequence 7442, Ap
10	70	10.3	337	10 US-09-014-777A-126	Sequence 126, Ap
11	70	10.3	340	10 US-09-814-777A-15	Sequence 15, Appli
12	70	10.3	384	10 US-09-814-777A-18	Sequence 18, Appli
13	70	10.3	384	10 US-09-814-777A-20	Sequence 20, Appli
14	70	10.3	470	10 US-09-814-777A-100	Sequence 100, Appli
15	70	10.3	680	12 US-10-369-93-3446	Sequence 3446, Ap

SEQUENCE CHARACTERISTICS:
 LENGTH: 129 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: Consensus
 CLONE: Consensus
 US-09-726-899-3

Query Match Score 678; DB 9; Length 129;
 Best Local Similarity 100.0%; Pred. No. 9.4e-73;
 Matches 129; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

Qy 1 MSFPKYKPSSSLRTLPETLDPAEYNISPETRAQERLAIRQLREYLYQYNDPNRRLI 60
 Dbs 1 MSFPKYKPSSSLRTLPETLDPAEYNISPETRAQERLAIRQLREYLYQYNDPNRRLI 60

Qy 61 ENPALLRWAYRTINTVYNPRPTPKNSLMGALCGFGLIFYYIKTERDRKEKLIQSGK 120
 Dbs 61 ENPALLRWAYRTINTVYNPRPTPKNSLMGALCGFGLIFYYIKTERDRKEKLIQSGK 120

Qy 121 LDRTFHLISY 129
 Dbs 121 LDRTFHLISY 129

RESULT 2
 US-10-264-049-3428
 Sequence 3428, Application US/10264049
 Publication No. US2004005579A1
 GENERAL INFORMATION:
 APPLICANT: Birse et al.
 TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 CURRENT APPLICATION NUMBER: US/10/264,049
 CURRENT FILING DATE: 2002-10-04
 PRIOR APPLICATION NUMBER: PCT/US01/18569
 PRIOR FILING DATE: 2001-06-07
 PRIOR APPLICATION NUMBER: US 60/209,467
 PRIOR FILING DATE: 2000-06-07
 NUMBER OF SEQ ID NOS: 4360
 SEQ ID NO 3428
 SOFTWARE: PatentIn ver. 3.1
 LENGTH: 117
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: MISC_FEATURE
 LOCATION: (3)
 OTHER INFORMATION: xaa equals any of the twenty naturally occurring L-amino acid
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 NAME/KEY: MISC_FEATURE
 LOCATION: (27)
 OTHER INFORMATION: xaa equals any of the twenty naturally occurring L-amino acid
 US-10-264-049-3428

Query Match Score 522; DB 12; Length 117;
 Best Local Similarity 99.0%; Pred. No. 3.2e-54;
 Matches 99; Conservative 0; Mismatches 1;
 Indels 0; Gaps 0;

Qy 2 SFPKYKPSSSLRTLPETLDPAEYNISPETRAQERLAIRQLREYLYQYNDPNRRLI 61
 Dbs 18 SFPKYKPSSSLRTLPETLDPAEYNISPETRAQERLAIRQLREYLYQYNDPNRRLI 77

Qy 62 NPALLRWAYRTINTVYNPRPTPKNSLMGALCGFGLIFYYIKTERDRKEKLIQSGK 101
 Dbs 78 NPALLRWAYRTINTVYNPRPTPKNSLMGALCGFGLIFYYIKTERDRKEKLIQSGK 117

RESULT 3
 US-09-726-899-10
 Sequence 10,
 Sequence 10,
 Application US/09726899

PRIOR FILING DATE: 2000-09-28
 PRIOR APPLICATION NUMBER: US 60/157,137
 PRIOR FILING DATE: 1999-09-29
 PRIOR APPLICATION NUMBER: US 60/163,280
 PRIOR FILING DATE: 1999-11-03
 NUMBER OF SEQ ID NOS: 8564
 SOFTWARE: PatentIn Ver. 3.0
 SEQ ID NO 4407
 LENGTH: 33
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-106-690-4407

Query Match 18.3%; Score 124; DB 15; Length 33;
 Best Local Similarity 100%; Pred. No. 1.6e-07;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 106 KTEDDRKEKLQI0EQGKLDRPHLSY 129
 Db 10 KTERDRKEKLQI0EQGKLDRPHLSY 33

RESULT 5

Sequence 1044, Application US/09925299
 Patent No. US20020056627A1
 GENERAL INFORMATION:
 APPLICANT: Rosen et al.
 TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
 FILE REFERENCE: PA102
 CURRENT APPLICATION NUMBER: US/09/925,299
 CURRENT FILING DATE: 2001-08-10
 PRIOR APPLICATION NUMBER: PCT/US00/05883
 PRIOR FILING DATE: 2000-03-08
 PRIOR APPLICATION NUMBER: 60/124,270
 NUMBER OF SEQ ID NOS: 1556
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 1044
 LENGTH: 16
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-925-299-1044

Query Match 11.2%; Score 76; DB 9; Length 16;
 Best Local Similarity 93.8%; Pred. No. 0.032;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 114 KLI0EQGKLDRPHLSY 129
 Db 1 KLI0VGLDRPHLSY 16

RESULT 6

Sequence 1144, Application US/09925299
 Patent No. US20030040517A9
 GENERAL INFORMATION:
 APPLICANT: Rosen et al.
 TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
 FILE REFERENCE: PA102
 CURRENT APPLICATION NUMBER: US/09/925,299
 CURRENT FILING DATE: 2001-08-10
 PRIOR APPLICATION NUMBER: PCT/US00/05883
 PRIOR FILING DATE: 2000-03-08
 PRIOR APPLICATION NUMBER: 60/124,270
 PRIOR FILING DATE: 1999-03-12
 NUMBER OF SEQ ID NOS: 1556
 SEQ ID NO 1044
 LENGTH: 16
 TYPE: PRT
 ORGANISM: Homo sapiens

Query Match 11.2%; Score 76; DB 11; Length 16;
 Best Local Similarity 93.8%; Pred. No. 0.032;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 114 KLI0EQGKLDRPHLSY 129
 Db 1 KLI0VGLDRPHLSY 16

RESULT 7

Sequence 21273, Application US/10369493
 Publication No. US20030233375A1
 GENERAL INFORMATION:
 APPLICANT: Cao, Yongwei
 APPLICANT: Hinkle, Gregory J.
 APPLICANT: Slater, Steven C.
 APPLICANT: Goldinan, Barry S.
 APPLICANT: Chen, Xianfeng
 TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF PLANTS WITH IMPROVED PROPERTIES
 FILE REFERENCE: 38-10(52052)B
 CURRENT APPLICATION NUMBER: US/10/369,493
 CURRENT FILING DATE: 2003-02-28
 PRIOR APPLICATION NUMBER: US 60/360,039
 NUMBER OF SEQ ID NOS: 47374
 SEQ ID NO 21273
 LENGTH: 433
 TYPE: PRT
 ORGANISM: Xenorhabdus nematophilus
 US-10-369-493-21273

Query Match 10.5%; Score 71; DB 12; Length 433;
 Best Local Similarity 20.3%; Pred. No. 9.9;
 Matches 24; Conservative 29; Mismatches 37; Indels 28; Gaps 5;

Qy 10 SLRTLPETLDPAEYNISPETRAQAERLTRAQLEGRYLQDNPNRGLIENPALLRWA 69
 Db 121 ALRTLPVLLDIAH-----KVERLAP-----WIFNSNP--AGVI-TEAVSRY 162

Query Match 70.9%; Score 70; DB 16; Length 70;
 Best Local Similarity 93.8%; Pred. No. 0.032;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 70 YARTI-----NVYPNFRPTKNSLGMALCGFGPLIIFYIITKTERDRKEKLQI 117
 Db 163 KAKLIGLCLNPVPSMEHMIAMLQRSYQDVLQRFAGLHMYWVHQVLVNGRDETEQVILE 220

RESULT 8

Sequence 2618, Application US/10369493
 Publication No. US20030233375A1
 GENERAL INFORMATION:
 APPLICANT: Cao, Yongwei
 APPLICANT: Hinkle, Gregory J.
 APPLICANT: Slater, Steven C.
 APPLICANT: Goldinan, Barry S.
 APPLICANT: Chen, Xianfeng
 TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF PLANTS WITH IMPROVED PROPERTIES
 FILE REFERENCE: 38-10(52052)B
 CURRENT APPLICATION NUMBER: US/10/369,493
 CURRENT FILING DATE: 2003-02-28
 PRIOR APPLICATION NUMBER: US 60/360,039
 PRIOR FILING DATE: 2002-02-21
 NUMBER OF SEQ ID NOS: 47374
 SEQ ID NO 2648
 LENGTH: 788
 TYPE: PRT
 ORGANISM: Synechocystis sp.
 US-10-369-493-2648

Query Match 10.4%; Score 70.5; DB 12; Length 788;

Best Local Similarity 30.5%; Pred. No. 25; Mismatches 9; Indels 33; Gaps 3; Matches 25; Conservative 9; Sequence 126, Application US/09814777A

Qy 16 ETLDPARYNISPETRRAQAEIRLAIHQKREYLQYDNPNRGLIENPALLRWAYARTI- 74
 Db 587 EILDSLEKDDERLDRQADLQDVLYELNREVRQDD-KSEEGFFE- -----AICKFT 638
 Qy 75 -----NVYPNRPRTPKNSLMG 90
 Db 639 GDFDDDDYDYNRRPAPRDPYRG 660

RESULT 9
 US-10-032-585-7442
 ; Sequence 7442, Application US/10032585
 ; GENERAL INFORMATION:
 ; APPLICANT: Terry, Roemer D.
 ; APPLICANT: Bo, Jiang
 ; APPLICANT: Charles, Boone
 ; APPLICANT: Howard, Bussey
 ; TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
 ; FILE REFERENCE: 10182-005-959
 ; CURRENT APPLICATION NUMBER: US/10/032,585
 ; CURRENT FILING DATE: 2001-12-20
 ; NUMBER OF SEQ ID NOS: 8000
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO: 7442
 ; LENGTH: 936
 ; TYPE: PRT
 ; ORGANISM: Candida albicans
 US-10-032-585-7442

Query Match Score 10.4%; Score 70.5; DB 12; Length 936;
 Best Local Similarity 29.2%; Pred. No. 31; Mismatches 14; Indels 25; Gaps 5; Matches 26; Conservative 14; Sequence 126, Application US/09814777A

Qy 6 YKPSSLRPTLPETDPARYNISPETRRAQAEIRLAIHQKREYL------QYN-DPNRR 57
 Db 118 YKPNAAITLSQLKUDPITRN-----AERLPKNAIVDKNPVISSAALISSYNNLPHAK 169
 Qy 58 GLIE--NPAELLRWAYARTINYVPNFRRT 83
 Db 170 EVVKRFTNETL-----ETIQSTSFKFP 192

RESULT 10
 US-09-814-777A-126
 ; Sequence 126, Application US/09814777A
 ; GENERAL INFORMATION:
 ; APPLICANT: KOOPMAN, Peter Anthony
 ; APPLICANT: MUSCAT, George Eugene Orlando
 ; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES AND METHODS OF USING THEM
 ; FILE REFERENCE: 21415-0003
 ; CURRENT APPLICATION NUMBER: US/09/814,777A
 ; PRIOR APPLICATION NUMBER: AU PQ6457
 ; PRIOR FILING DATE: 2000-03-24
 ; NUMBER OF SEQ ID NOS: 128
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO: 126
 ; LENGTH: 337
 ; TYPE: PRT
 ; ORGANISM: Human
 US-09-814-777A-126

Query Match Score 10.3%; Score 70; DB 10; Length 337;
 Best Local Similarity 20.8%; Pred. No. 9 4; Mismatches 21; Indels 54; Gaps 5; Matches 31; Conservative 21; Sequence 126, Application US/09814777A

Qy 4 PKYKPSSURTLPTLDPPABYNISPETR--RAQAEIRLAI-----AQKREYLLQYN 52
 Db 64 PDLHNAVLSKMLGKAWKELNAEKRPPVEAERLVOHLRD--HENYKYPFR- -----113
 Qy 93 CGFGPLIIFYIYIKTERDRKEKLQIPEGKL 121
 Db 114 -----RKQKARKARRLBPGL 129

RESULT 11
 US-09-814-777A-15
 ; Sequence 15, Application US/09814777A
 ; Patent No. US20020142415A1
 ; GENERAL INFORMATION:
 ; APPLICANT: KOOPMAN, Peter Anthony
 ; APPLICANT: MUSCAT, George Eugene Orlando
 ; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES AND METHODS OF USING THEM
 ; FILE REFERENCE: 21415-0003
 ; CURRENT APPLICATION NUMBER: US/09/814,777A
 ; PRIOR APPLICATION NUMBER: AU PQ6457
 ; PRIOR FILING DATE: 2000-03-24
 ; NUMBER OF SEQ ID NOS: 128
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO: 15
 ; LENGTH: 340
 ; TYPE: PRT
 ; ORGANISM: Human
 US-09-814-777A-15

Query Match Score 10.3%; Score 70; DB 10; Length 340;
 Best Local Similarity 20.8%; Pred. No. 9 5; Mismatches 43; Indels 54; Gaps 5; Matches 31; Conservative 21; Sequence 126, Application US/09814777A

Qy 4 PKYKPSSURTLPTLDPPABYNISPETR--RAQAEIRLAI-----AQKREYLLQYN 52
 Db 4 PASKPSQSPRSPPRSPPBGRGLSPAGRGERQADESIRRPMPNAFWAKDERLRAQON 63
 Qy 53 D-----PWRGLIENPALLRWAYARTINYVPNFRTPKNSLMGAL 92
 Db 64 PDLHNAVLSKMLGKAWKELNAEKRPPVEAERLVOHLRD--HENYKYPFR- -----113
 Qy 93 CGFGPLIIFYIYIKTERDRKEKLQIPEGKL 121
 Db 114 -----RKQKARKARRLBPGL 129

RESULT 12
 US-09-814-777A-18
 ; Sequence 18, Application US/09814777A
 ; Patent No. US20020142415A1
 ; GENERAL INFORMATION:
 ; APPLICANT: KOOPMAN, Peter Anthony
 ; APPLICANT: MUSCAT, George Eugene Orlando
 ; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES AND METHODS OF USING THEM
 ; FILE REFERENCE: 21415-0003
 ; CURRENT APPLICATION NUMBER: US/09/814,777A
 ; PRIOR APPLICATION NUMBER: AU PQ6457
 ; PRIOR FILING DATE: 2000-03-24
 ; NUMBER OF SEQ ID NOS: 128
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO: 18
 ; LENGTH: 384
 ; TYPE: PRT
 ; ORGANISM: Human
 US-09-814-777A-18

Query Match Score 10.3%; Score 70; DB 10; Length 384;
 Best Local Similarity 20.8%; Pred. No. 9 4; Mismatches 21; Indels 54; Gaps 5; Matches 31; Sequence 126, Application US/09814777A

Qy 4 PKYKPSSURTLPTLDPPABYNISPETR--RAQAEIRLAI-----AQKREYLLQYN 52
 Db 64 PDLHNAVLSKMLGKAWKELNAEKRPPVEAERLVOHLRD--HENYKYPFR- -----113
 Qy 93 CGFGPLIIFYIYIKTERDRKEKLQIPEGKL 121
 Db 114 -----RKQKARKARRLBPGL 129

OTHER INFORMATION: Exon 2
 US-09-814-777A-18
 Query Match 10.3%; Score 70; DB 10; Length 384;
 Best Local Similarity 20.8%; Pred. No. 11;
 Matches 31; Conservative 21; Mismatches 43; Indels 54; Gaps 5;
 Qy 4 PKYKPPSSLRLTPETDPAEYNISPTR-RAQAERLAI R-----AQLKREYLQVN 52
 Db 48 PASPPSPQRSPPRSPBPGYGLSPAGRGEQQADESRRPMAFMWKADEKRLAQVN 107
 Qy 53 D-----PNEGRGLIENPALLRWAYARTINYTPNFRTPKNSLMGAL 92
 Db 108 PDLMIAVLSKMLGKAWKELNAAEKRPFVBEAERLVRQHLD--HPNYKTRPR---- 157
 Qy 93 CGFGPLIIFYIILKTERDKEKLIQEGKL 121
 Db 158 -----RKKQARKARRLEPGKL 173

RESULT 13

US-09-814-777A-20

Sequence 20, Application US/09814777A

Patent No. US2002014415A1

GENERAL INFORMATION:

APPLICANT: KOOPMAN, Peter Anthony

INVENTOR: MUSCAT, George Eugene Orlando

TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES AND METHODS OF USING THEM

FILE REFERENCE: 214-5-0003

CURRENT APPLICATION NUMBER: US/09/814,777A

CURRENT FILING DATE: 2001-03-23

PRIOR APPLICATION NUMBER: AU/BQ6457

PRIOR FILING DATE: 2000-03-24

NUMBER OF SEQ ID NOS: 128

SOFTWARE: PatentIn version 3.0

SEQ ID NO 20

LENGTH: 384

TYPE: PRT

ORGANISM: Human

US-09-814-777A-20

Query Match 10.3%; Score 70; DB 10; Length 384;
 Best Local Similarity 20.8%; Pred. No. 11;
 Matches 31; Conservative 21; Mismatches 43; Indels 54; Gaps 5;

Qy 4 PKYKPPSSLRLTPETDPAEYNISPTR-RAQAERLAI R-----AQLKREYLQVN 52
 Db 48 PASPPSPQRSPPRSPBPGYGLSPAGRGEQQADESRRPMAFMWKADEKRLAQVN 107
 Qy 53 D-----PNEGRGLIENPALLRWAYARTINYTPNFRTPKNSLMGAL 92
 Db 108 PDLMIAVLSKMLGKAWKELNAAEKRPFVBEAERLVRQHLD--HPNYKTRPR---- 157
 Qy 93 CGFGPLIIFYIILKTERDKEKLIQEGKL 121
 Db 158 -----RKKQARKARRLEPGKL 173

RESULT 14

US-09-814-777A-100

Sequence 100, Application US/09814777A

Patent No. US20020142415A1

GENERAL INFORMATION:

APPLICANT: KOOPMAN, Peter Anthony

INVENTOR: MUSCAT, George Eugene Orlando

TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES AND METHODS OF USING THEM

FILE REFERENCE: 14-15-003

CURRENT APPLICATION NUMBER: US/09/814,777A

CURRENT FILING DATE: 2001-03-23

PRIOR APPLICATION NUMBER: AU/P06457

NUMBER OF SEQ ID NOS: 128

SOFTWARE: PatentIn version 3.0

Search completed: January 29, 2004, 09:14:04

Job time : 34 secs

OTHER INFORMATION: Exon 2
 US-09-814-777A-18
 Query Match 10.3%; Score 70; DB 10; Length 470;
 Best Local Similarity 20.8%; Pred. No. 15;
 Matches 31; Conservative 21; Mismatches 43; Indels 54; Gaps 5;
 Qy 4 PKYKPPSSLRLTPETDPAEYNISPTR-RAQAERLAI R-----AQLKREYLQVN 52
 Db 4 PASPPSPQRSPPRSPBPGYGLSPAGRGEQQADESRRPMAFMWKADEKRLAQVN 63
 Qy 53 D-----PNEGRGLIENPALLRWAYARTINYTPNFRTPKNSLMGAL 92
 Db 4 PASPPSPQRSPPRSPBPGYGLSPAGRGEQQADESRRPMAFMWKADEKRLAQVN 63
 Qy 53 D-----PNEGRGLIENPALLRWAYARTINYTPNFRTPKNSLMGAL 92
 Db 64 PDLHNAVLSKMLGKAWKELNAAEKRPFVBEAERLVRQHLD--HPNYKTRPR---- 113
 Qy 93 CGFGPLIIFYIILKTERDKEKLIQEGKL 121
 Db 114 -----RKKQARKARRLEPGKL 129

RESULT 15

US-10-369-493-3446

Sequence 3446, Application US/10369493

GENERAL INFORMATION:

PUBLICATION NO. US20030233375A1

APPLICANT: Cao, Yongwei

APPLICANT: Hinkle, Gregory J.

APPLICANT: Slater, Steven C.

APPLICANT: Goldman, Barry S.

APPLICANT: Chen, Xianfeng

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF PLANTS WITH IMPROVED PROPERTIES

TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

FILE REFERENCE: 38-10/52052(B)

CURRENT APPLICATION NUMBER: US/10/369,493

CURRENT FILING DATE: 2003-02-28

PRIOR APPLICATION NUMBER: US 60/360,039

PRIOR FILING DATE: 2002-02-21

NUMBER OF SEQ ID NOS: 47374

SEQ ID NO: 3446

LENGTH: 680

TYPE: PRT

ORGANISM: Neurospora crassa

US-10-369-493-3446

Query Match 10.3%; Score 70; DB 12; Length 680;

Best Local Similarity 23.2%; Pred. No. 24;

Matches 35; Conservative 18; Mismatches 36; Indels 62; Gaps 6;

Qy 4 PKYKPPSSLRLTPETDPAEYNISPTR-RAQAERLAI R-----AQLKREYLQVN 52

Db 241 PRREPLTPLPDEPVISQMTGFKFGPEYTAELTRIKSPKQAAVRLEKERPEPIA 300

Qy 39 IAAQRREYLQYNDPNRRLIENPALLRWAYARTINYTPNFRTPKNSLNGA-----91

Db 301 KDAEKKRGFGFDF-----YKRANSV-----TSKDTLTAASSSEGSL 336

Qy 92 -----LCGFGPLIIFYIILKTERDKEKLI 116

Db 337 GDDPNAFDPLSITYLVRETLERBNHVT 367

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OM protein - protein search, using bw model

Run on: January 29, 2004, 09:05:56 ; Search time 22 Seconds (without alignments)
248.095 Million cell. updates/sec

Title: US-09-726-899-3
Sequence: 1 MSFPYKPKSSIRLTLPTLDP.....DRKEKLHQEGKLDRPFHLSY 129

Perfect score: 678

Scoring table: BLOSUM62
Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : Issued Patents AA:*

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2: /cgns2_6/podata/1/iaa/5B_COMB.pep:*

3: /cgns2_6/podata/1/iaa/6A_COMB.pep:*

4: /cgns2_6/podata/1/iaa/6B_COMB.pep:*

5: /cgns2_6/podata/1/iaa/pcetus_COMB.pep:*

6: /cgns2_6/podata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	678	100.0	129	2 US-09-785-065-3	Sequence 3, Appli
2	678	100.0	129	4 US-09-151-912-3	Sequence 3, Appli
3	514	75.8	129	2 US-08-785-065-10	Sequence 10, Appli
4	514	75.8	129	4 US-09-151-912-10	Sequence 10, Appli
5	79	11.7	346	4 US-09-252-991A-24156	Sequence 24156, A
6	70	10.3	360	4 US-09-252-991A-17420	Sequence 17420, A
7	69.5	10.3	294	2 US-08-874-947-26	Sequence 26, Appli
8	69.5	10.3	294	3 US-09-093-922-26	Sequence 26, Appli
9	69.5	10.3	354	4 US-09-252-991A-28779	Sequence 28779, A
10	69	10.2	640	4 US-09-592-555A-2	Sequence 2, Appli
11	69	10.2	640	4 US-09-592-995A-4	Sequence 4, Appli
12	69	10.2	656	3 US-08-738-000-3	Sequence 4, Appli
13	69	10.2	656	3 US-09-258-938-4	Sequence 4, Appli
14	69	10.2	656	4 US-09-347-878-24	Sequence 24, Appli
15	69	10.2	656	4 US-09-660-872A-4	Sequence 4, Appli
16	69	10.2	660	3 US-08-738-000-2	Sequence 2, Appli
17	69	10.2	660	3 US-09-258-928-2	Sequence 2, Appli
18	69	10.2	660	4 US-09-660-872A-2	Sequence 2, Appli
19	68	10.0	196	4 US-09-227-377-393	Sequence 393, App
20	68	10.0	228	4 US-09-227-377-401	Sequence 401, App
21	68	10.0	371	4 US-09-199-637A-295	Sequence 295, App
22	68	10.0	371	4 US-09-252-991A-21430	Sequence 21430, A
23	68	10.0	864	4 US-09-604-978-11	Sequence 11, Appli
24	68	10.0	864	4 US-09-604-978-11	Sequence 11, Appli
25	67.5	10.0	603	4 US-09-252-991A-311905	Sequence 311905, A
26	66.5	9.8	1036	4 US-09-252-991A-18349	Sequence 18349, A
66	9.7				Sequence 26493, A

ALIGNMENTS

RESULT 1
US-09-785-065-3
; Sequence 3, Application US/08785065
; Patent No. 5814451
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: NOVEL SUBUNITS OF NADH DEHYDROGENASE
; NUMBER OF SEQUENCES: 12
; CORESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3114 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/785,065
; FILING DATE: Herewith
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0187 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 129 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: Consensus
; CLONE: Consensus
; US-08-785-065-3
Query Match Score 678; DB 2; Length 129;
Best Local Similarity 100.0%; Pred. No. 1.1e-74;

US-09-151-412-10
 ; Sequence 10, Application US/09151412
 ; Patent No. 6399345
 ; GENERAL INFORMATION:
 ; APPLICANT: Bandman, Olga
 ; APPLICANT: Goli, Surya K.
 ; APPLICANT: Hillman, Jennifer L.
 ; TITLE OF INVENTION: NOVEL SUBUNITS OF NADH DEHYDROGENASE
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.
 ; STREET: 3174 Porter Drive
 ; CITY: Palo Alto
 ; STATE: CA
 ; ZIP: 94304 USA
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/151,412
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/785,065
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Billings, Lucy J.
 ; REGISTRATION NUMBER: 36,749
 ; REFERENCE/DOCKET NUMBER: PF-0187 US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-845-0555
 ; TELEFAX: 415-845-4166
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 10:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 129 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; IMMEDIATE SOURCE:
 ; LIBRARY: GenBank
 ; CLONE: 114
 ; US-09-151-412-10

Query Match 75.8%; Score 514; DB 4; Length 129;
 Best Local Similarity 73.6%; Pred. No. 9e-55;
 Matches 95; Conservative 18; Mismatches 16; Indels 0; Gaps 0;

Qy 1 MSFPKYPSSURTLPTLDAEYNISPETRAAERLAIARQLKREYLQYNDPNRGLI 60
 Db 1 MSFPKYEASRSLSSLPTLDAEYDISSETRAQAAERLAIATSLRQLREYQYDPSRRGVI 60
 Qy 61 ENPALLRWAARTINYPNFRPTPKNSLMLGALCFPLIFYYIKTERKERKLIQEKG 120
 Db 61 EDPALVRYTARSANITYPNFRPTKTSLLGALFGIQLFWYYVFTDRKERKLIQEKG 120
 Qy 121 LDRTPHLSY 129
 Db 121 LDRTPNISY 129

RESULT 5
 US-09-252-991A-24156
 ; Sequence 24156, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS AND THERAPEUTICS
 ; FILE REFERENCE: 10196.136

Query Match 11.7%; Score 79; DB 4; Length 346;
 Best Local Similarity 37.5%; Pred. No. 0.22;
 Matches 21; Conservative 5; Mismatches 22; Indels 8; Gaps 1;

Qy 13 TLPEALDPANISPETRAAERLAIARQLKREYLQYNDPNRGLIENPALLRW 68
 Db 92 TLPEALDA-----RRAAGWRLACQCRVLSLVLQPPDPERDGLPARVYACHW 139

RESULT 6
 US-09-252-991A-17420
 ; Sequence 17420, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS AND THERAPEUTICS
 ; FILE REFERENCE: 107196.136

Query Match 10.3%; Score 70; DB 4; Length 360;
 Best Local Similarity 26.0%; Pred. No. 2.9;
 Matches 34; Conservative 17; Mismatches 52; Indels 28; Gaps 6;

Qy 15 PETLDPAEYNISPETRAAERLAIARQLKREYLQYNDPNRGLIENPALLRWAYR-- 72
 Db 202 PPAIDPDEV-----EQKKAHERVMARLQASIDLAQH-EPKSVVLLGHGTGAYWA-ARYL 253
 Qy 73 -----TINVYPNFRPKNSLMLGALCFPLIFYYIKTERDRKERKLIQE 118
 Db 254 AEKEPAEIHNLVLLTAEVPRDPRPALEDMPKLKLATGD-FYYRNDARADREARLRMOA 311

Query Match 11.9 GKLDTFHLSY 129
 Db 312 GK--RQHPAY 320

RESULT 7
 US-08-874-347-26
 ; Sequence 26, Application US/08874347
 ; Patent No. 5863741
 ; GENERAL INFORMATION:
 ; APPLICANT: Linper, Andrew H.
 ; APPLICANT: Leof, Edward B.
 ; APPLICANT: Thomas, Charles F.
 ; APPLICANT: Gustafson, Michael P.
 ; TITLE OF INVENTION: CD22 PROTEIN KINASE FROM PNEUMOCYSTIS CARINII
 ; NUMBER OF SEQUENCES : 26

CORRESPONDENCE ADDRESS:
 ADDRESS: Fish & Richardson P.C., P.A.
 STREET: 60 South Sixth Street, Suite 3300
 CITY: Minneapolis
 STATE: MN
 COUNTRY: USA
 ZIP: 55402

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/874,347
 FILING DATE: 13-JUN-1997
 CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
 NAME: Billinger, Mark S.
 REGISTRATION NUMBER: 34,812
 REFERENCE/DOCKET NUMBER: 07039/055001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 612-335-5070
 TELEFAX: 612-288-9696
 TELEX:
 INFORMATION FOR SEQ ID NO: 26:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 294 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein

US-08-874-347-26

Query Match Score 69.5; DB 2; Length 294;
 Best Local Similarity 36.2%; Pred. No. 2,5;
 Matches 17; Conservative 9; Mismatches 20; Indels 1; Gaps 1;

Qy 2 SPPKYKPSLSRLPTELDPDAEN-ISPETRRAQERLAIHQKREY 47
 Db 240 APPKWAQDLATIVPTLDPAIDLSSKMLRYEPNKRITARQALEHEY 286

RESULT 8
 US-09-093-522-26
 Sequence 26, Application US/09093522
 Patent No. 6015700

GENERAL INFORMATION:
 APPLICANT: Limer, Andrew H.
 APPLICANT: Leof, Edward B.
 APPLICANT: Thomas, Charles F.
 APPLICANT: Gustafson, Michael P.
 APPLICANT: Gustafson, Michael P.
 TITLE OF INVENTION: CDC2 PROTEIN KINASE FROM PNEUMOCYSTS
 TITLE OF INVENTION: CARINI
 NUMBER OF SEQUENCES: 26
 CORRESPONDENCE ADDRESS:
 ADDRESS: Fish & Richardson P.C., P.A.
 STREET: 60 South Sixth Street, Suite 3300
 CITY: Minneapolis
 STATE: MN
 COUNTRY: USA
 ZIP: 55402

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/093,522
 FILING DATE: 08-JUN-1998
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/874,347
 FILING DATE: 13-JUN-1997

ATTORNEY/AGENT INFORMATION:
 NAME: Billinger, Mark S.
 REGISTRATION NUMBER: 34,812
 REFERENCE/DOCKET NUMBER: 07039/055002
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 612-335-5070
 TELEFAX: 612-288-9696
 TELEX:
 INFORMATION FOR SEQ ID NO: 26:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 294 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein

US-09-093-522-26

Query Match Score 69.5; DB 3; Length 294;
 Best Local Similarity 36.2%; Pred. No. 2,5;
 Matches 17; Conservative 9; Mismatches 20; Indels 1; Gaps 1;

Qy 2 SPPKYKPSLSRLPTELDPABYN-ISPETRRAQERLAIHQKREY 47
 Db 240 APPKWAQDLATIVPTLDPAIDLSSKMLRYEPNKRITARQALEHEY 286

RESULT 9
 US-09-252-991A-28779
 Sequence 28779, Application US/09252991A
 Patent No. 6551795

GENERAL INFORMATION:
 APPLICANT: Marc J. Rubenfield et al.
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 FILE REFERENCE: 107196.136
 CURRENT APPLICATION NUMBER: US/09/252,991A
 PRIOR APPLICATION NUMBER: US 60/074,788
 PRIOR FILING DATE: 1999-02-18
 PRIOR APPLICATION NUMBER: US 60/094,190
 PRIOR FILING DATE: 1998-07-27
 NUMBER OF SEQ ID NOS: 33142
 SEQ ID NO 28779
 LENGTH: 354
 TYPE: PRT
 ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-28779

Query Match Score 69.5; DB 4; Length 354;
 Best Local Similarity 30.1%; Pred. No. 3,2;
 Matches 28; Conservative 12; Mismatches 36; Indels 17; Gaps 5;

Qy 7 KPSSSLRLPTELDPAEVNISPETRRAQERLAIHQKREYLNQYNDPNRGLIENPALL 66
 Db 142 RPDALPRIP--VDSHRSIGGVPGAHDRLLRRV-VRAGLRR-----GDPRR---DPAH 187

RESULT 10
 US-09-592-595A-2
 Sequence 2, Application US/09592595A
 Patent No. 6566065

GENERAL INFORMATION:
 APPLICANT: ROZEN, Rima
 TITLE OF INVENTION: cDNA FOR HUMAN METHYLENETETRAHYDROFOLATE
 FILE REFERENCE: 04844/005003
 CURRENT APPLICATION NUMBER: US/09/592,595A
 PRIOR APPLICATION NUMBER: 04844/005003
 CURRENT FILING DATE: 2000-06-12
 PRIOR APPLICATION NUMBER: US 09/258,928

PRIOR FILING DATE: 1999-03-01
 PRIOR APPLICATION NUMBER: US 09/738,000
 PRIOR FILING DATE: 1997-02-12
 PRIOR APPLICATION NUMBER: PCT/CA95/00314
 PRIOR FILING DATE: 1995-05-25
 PRIOR APPLICATION NUMBER: PCT/CA95/00314
 PRIOR FILING DATE: 1994-05-26
 PRIOR FILING DATE: 1994-05-26
 NUMBER OF SEQ ID NOS: 18
 SEQ ID NO: 2
 SOFTWARE: FastSEQ for Windows Version 4.0
 LENGTH: 660
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-592-595A-2

Query Match 10.2%; Score 69; DB 4; Length 640;
 Best Local Similarity 28.7%; Pred. No. 8.2;
 Matches 29; Conservative 14; Mismatches 32; Indels 26; Gaps 6;

Qy 35 ERLAIAQLKREYLQYNDPNRGLTENPALLRWAYARTINYPNFRPTPKNSLMGALCG 94
 Db 462 EPLAAETSLKKEBLRV--NRQGIL--TINSQPNINGKPSSD---PIVG 503

Qy 95 FGP---LIF--IYIILKTERDRKEKLQ--EGKLDRTFHL 127
 Db 504 WGPSSGGYVFKQAYLEFFTSRTEAALIQLKXCYELRYNH 544

RESULT 11
 US-09-592-595A-4
 Patent No. 6566065
 Sequence 4, Application US/09592595A
 GENERAL INFORMATION:
 APPLICANT: ROZEN, Rima
 TITLE OF INVENTION: cDNA FOR HUMAN METHYLENETETRAHYDROFOLATE
 FILE REFERENCE: 04844/005003
 CURRENT APPLICATION NUMBER: US/09/592,595A
 CURRENT FILING DATE: 2000-06-12
 PRIOR FILING NUMBER: US 09/258,928
 PRIOR FILING DATE: 1999-03-01
 PRIOR APPLICATION NUMBER: US 08/738,000
 PRIOR FILING DATE: 1997-02-12
 PRIOR APPLICATION NUMBER: PCT/CA95/00314
 PRIOR FILING DATE: 1995-05-25
 PRIOR APPLICATION NUMBER: GB 9410620.0
 NUMBER OF SEQ ID NOS: 18
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 4
 LENGTH: 656
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-592-595A-4

Query Match 10.2%; Score 69; DB 4; Length 640;
 Best Local Similarity 28.7%; Pred. No. 8.2;
 Matches 29; Conservative 14; Mismatches 32; Indels 26; Gaps 6;

Qy 35 ERLAIAQLKREYLQYNDPNRGLTENPALLRWAYARTINYPNFRPTPKNSLMGALCG 94
 Db 458 EPLAAETSLKKEBLRV--NRQGIL--TINSQPNINGKPSSD---PIVG 499

Qy 95 FGP---LIF--IYIILKTERDRKEKLQ--EGKLDRTFHL 127
 Db 500 WGPSSGGYVFKQAYLEFFTSRTEAALIQLKXCYELRYNH 544

RESULT 12
 US-09-258-928-4
 Sequence 4, Application US/09258928
 Patent No. 6218120
 GENERAL INFORMATION:
 APPLICANT: GOYTEBE, Philippe
 TITLE OF INVENTION: cDNA FOR HUMAN METHYLENETETRAHYDROFOLATE
 FILE REFERENCE: 04844/005002
 CURRENT APPLICATION NUMBER: US/09/258,928
 PRIOR APPLICATION NUMBER: 08/738,000
 PRIOR FILING DATE: 1997-02-12
 PRIOR APPLICATION NUMBER: GB 9410620.0
 PRIOR FILING DATE: 1994-05-26
 NUMBER OF SEQ ID NOS: 14
 SEQ ID NO: 4
 LENGTH: 656
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-258-928-4

Query Match 10.2%; Score 69; DB 3; Length 656;
 Best Local Similarity 28.7%; Pred. No. 8.5;
 Matches 29; Conservative 14; Mismatches 32; Indels 26; Gaps 6;

Qy 35 ERLAIAQLKREYLQYNDPNRGLTENPALLRWAYARTINYPNFRPTPKNSLMGALCG 94
 Db 458 EPLAAETSLKKEBLRV--NRQGIL--TINSQPNINGKPSSD---PIVG 499

Qy 95 FGP---LIF--IYIILKTERDRKEKLQ--EGKLDRTFHL 127
 Db 500 WGPSSGGYVFKQAYLEFFTSRTEAALIQLKXCYELRYNH 544

RESULT 13
 US-09-258-928-4
 Sequence 4, Application US/09258928
 Patent No. 6218120
 GENERAL INFORMATION:
 APPLICANT: ROZEN, Rima
 TITLE OF INVENTION: cDNA FOR HUMAN METHYLENETETRAHYDROFOLATE
 FILE REFERENCE: 04844/005002
 CURRENT FILING DATE: 1999-03-01
 PRIOR APPLICATION NUMBER: 08/738,000
 PRIOR FILING DATE: 1997-02-12
 PRIOR APPLICATION NUMBER: GB 9410620.0
 PRIOR FILING DATE: 1994-05-26
 NUMBER OF SEQ ID NOS: 14
 SEQ ID NO: 4
 LENGTH: 656
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-258-928-4

Query Match 10.2%; Score 69; DB 3; Length 656;
 Best Local Similarity 28.7%; Pred. No. 8.5;
 Matches 29; Conservative 14; Mismatches 32; Indels 26; Gaps 6;

RESULT 14
 US-09-347-878-24
 Sequence 24, Application US/09347878C
 Patent No. 6378210
 GENERAL INFORMATION:
 APPLICANT: Yuan, Chong
 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ASSAYING ANALYTES
 FILE REFERENCE: 25385-1651
 CURRENT APPLICATION NUMBER: US/09/347,878C
 NUMBER OF SEQ ID NOS: 75
 CURRENT FILING DATE: 1999-07-06
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 24
 LENGTH: 656
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE: OTHER INFORMATION: Human methylenetetrahydrofolate reductase (MTHFR)
 OTHER INFORMATION: Protein sequence
 PUBLICATION INFORMATION:
 DATABASE ACCESSION NUMBER: AP105977/GenBank 1-11
 US-09-347-878-24

Query Match 35 ERЛАIAQKREYLQNDPNRGLIENPALLRWAYARTINYVPNFRPTPKNSLGMALCG 94
 Best Local Similarity 28.7%; Pred. No. 8.5%;
 Mismatches 14; Indels 32; Gaps 6;
 Matches 29; Conservative 14; MisMatches 32; Indels 26; Gaps 6;

Qy 35 ERЛАIAQKREYLQNDPNRGLIENPALLRWAYARTINYVPNFRPTPKNSLGMALCG 94
 Db 458 EPLAAETSLKKEELRV---NRQGIL-----TINSQNPINGKPSSD---P1VG 499

RESULT 14
 US-09-347-878-24
 Sequence 24, Application US/09347878C
 Patent No. 6378210
 GENERAL INFORMATION:
 APPLICANT: Yuan, Chong
 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ASSAYING ANALYTES
 FILE REFERENCE: 25385-1651
 CURRENT APPLICATION NUMBER: US/09/347,878C
 NUMBER OF SEQ ID NOS: 75
 CURRENT FILING DATE: 1999-07-06
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 24
 LENGTH: 656
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE: OTHER INFORMATION: Human methylenetetrahydrofolate reductase (MTHFR)
 OTHER INFORMATION: Protein sequence
 PUBLICATION INFORMATION:
 DATABASE ACCESSION NUMBER: AP105977/GenBank 1-11
 US-09-347-878-24

Query Match 35 ERЛАIAQKREYLQNDPNRGLIENPALLRWAYARTINYVPNFRPTPKNSLGMALCG 94
 Best Local Similarity 28.7%; Pred. No. 8.5%;
 Mismatches 14; Indels 32; Gaps 6;
 Matches 29; Conservative 14; MisMatches 32; Indels 26; Gaps 6;

Qy 35 ERЛАIAQKREYLQNDPNRGLIENPALLRWAYARTINYVPNFRPTPKNSLGMALCG 94
 Db 458 EPLAAETSLKKEELRV---NRQGIL-----TINSQNPINGKPSSD---P1VG 499

RESULT 15
 US-09-660-872A-4
 Sequence 4, Application US/09660872A
 Patent No. 6528259
 GENERAL INFORMATION:
 APPLICANT: GOYETTE, Philippe
 APPLICANT: ROZEN, Fima
 TITLE OF INVENTION: cDNA: FOR HUMAN METHYLENETETRAHYDROFOLATE
 REDUCTASE
 TITLE OF INVENTION: REDUCTASE
 FILE REFERENCE: 0484/005004
 CURRENT FILING DATE: 2000-09-13
 PRIOR APPLICATION NUMBER: PCT/IB00/00442
 PRIOR FILING DATE: 2000-02-28
 PRIOR APPLICATION NUMBER: US 09/258,928
 PRIOR FILING DATE: 1999-03-01
 PRIOR APPLICATION NUMBER: US 08/738,000
 PRIOR FILING DATE: 1997-02-12
 PRIOR APPLICATION NUMBER: PCT/CA95/00314
 PRIOR FILING DATE: 1995-05-25
 PRIOR APPLICATION NUMBER: GB 9410620.0
 PRIOR FILING DATE: 1994-05-26
 NUMBER OF SEQ ID NOS: 18
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 4
 LENGTH: 656
 TYPE: PRT

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OM protein - protein search, using sw model

Run on: January 29, 2004, 09:14:07 ; Search time 20 Seconds
(without alignments)

620.288 Million cell updates/sec

Title: US-09-726-899-3
Sequence: 1 MSPPTKPSSURTLPTLDP.....DEKEKLIOBKGKUDRTHFLSY 129

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 75 summaries

Database : PIR 76:*

1: Piri1:*

2: Piri2:*

3: Piri3:*

4: Piri4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	129	100.0	129	2	JB0383		NADH2 dehydrogenase (ubiquinone) (BC 1.6.5.3) Chain NDUFB4 - human
2	17	13.2	129	2	S28237		NADH:ubiquinone oxidoreductase subunit NDUFB4
3	8	6.2	133	2	JC2003		NADH:ubiquinone oxidoreductase subunit NDUFB4
4	8	6.2	160	2	B71176		NADH:ubiquinone oxidoreductase subunit NDUFB4
5	8	6.2	179	2	A33164		NADH:ubiquinone oxidoreductase subunit NDUFB4
6	8	6.2	244	2	AB1318		NADH:ubiquinone oxidoreductase subunit NDUFB4
7	8	6.2	244	2	AB1690		NADH:ubiquinone oxidoreductase subunit NDUFB4
8	8	6.2	451	2	HB2042		NADH:ubiquinone oxidoreductase subunit NDUFB4
9	8	6.2	466	2	B95262		NADH:ubiquinone oxidoreductase subunit NDUFB4
10	8	6.2	468	2	BB3046		NADH:ubiquinone oxidoreductase subunit NDUFB4
11	8	6.2	658	2	T40107		NADH:ubiquinone oxidoreductase subunit NDUFB4
12	8	6.2	1440	1	SYHUQT		NADH:ubiquinone oxidoreductase subunit NDUFB4
13	7	5.4	127	2	AH0316		NADH:ubiquinone oxidoreductase subunit NDUFB4
14	7	5.4	227	2	T22144		NADH:ubiquinone oxidoreductase subunit NDUFB4
15	7	5.4	239	2	AD0088		NADH:ubiquinone oxidoreductase subunit NDUFB4
16	7	5.4	252	2	D95266		NADH:ubiquinone oxidoreductase subunit NDUFB4
17	7	5.4	278	2	C41841		NADH:ubiquinone oxidoreductase subunit NDUFB4
18	7	5.4	278	2	AD1872		NADH:ubiquinone oxidoreductase subunit NDUFB4
19	7	5.4	282	2	AC2047		NADH:ubiquinone oxidoreductase subunit NDUFB4
20	7	5.4	310	2	T36068		NADH:ubiquinone oxidoreductase subunit NDUFB4
21	7	5.4	321	2	GB2688		NADH:ubiquinone oxidoreductase subunit NDUFB4
22	7	5.4	347	2	T31205		NADH:ubiquinone oxidoreductase subunit NDUFB4
23	7	5.4	366	2	C87624		NADH:ubiquinone oxidoreductase subunit NDUFB4
24	7	5.4	398	2	F90206		NADH:ubiquinone oxidoreductase subunit NDUFB4
25	7	5.4	400	2	T27952		NADH:ubiquinone oxidoreductase subunit NDUFB4
26	7	5.4	438	2	G96035		NADH:ubiquinone oxidoreductase subunit NDUFB4
27	7	5.4	587	2	I40849		NADH:ubiquinone oxidoreductase subunit NDUFB4
28	7	5.4	608	2	A64992		NADH:ubiquinone oxidoreductase subunit NDUFB4
29	7	5.4	628	2	S77374		NADH:ubiquinone oxidoreductase subunit NDUFB4

ALIGNMENTS

RESULT 1

JB0383

NADH2 dehydrogenase (ubiquinone) (BC 1.6.5.3) Chain NDUFB4 - human

NADH:ubiquinone oxidoreductase subunit NDUFB4

N;Alternate names: NADH:ubiquinone oxidoreductase subunit NDUFB4

C;Species: Homo sapiens (man)

C;Accession: JB0383

R;Loeffen, J.L.C.M.; Triepels, R.H.; van den Heuvel, L.P.; Schuelke, M.; Buskens, C.A.; Biochem. Biophys. Res. Commun. 253, 415-422, 1998

A;Title: CDNA of eight nuclear encoded subunits of NADH:ubiquinone oxidoreductase: Hum

A;Reference number: JB0379; MUID:93097250; PMID:9818551

A;Accession: JB0383

A;Status: Preliminary

A;Molecule type: mRNA

A;Residues: 1-129 <LOB>

A;Cross-reference: GB:AF044957; NID:94164445; PID:AAD05421.1; PMID:94164446

C;Keywords: NADH:ubiquinone oxidoreductase

Query Match 100.0%

Best Local Similarity 100.0%

Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Score 129; DB 2; Length 129;

Pred. No. 2.5e-126;

Prob. 3-hydroxy

succinate dehydro

sensor protein Ata

cell division prot

Qy 1 MSPPKPKSSSLRTPETLPAETNISPTERRAQERLAIRQLKREYVLLQYNDPNNRGLI 60

Db 1 MSFPKPKSSSLRTPETLPAETNISPTERRAQERLAIRQLKREYVLLQYNDPNNRGLI 60

C;Species: Pyrococcus horikoshii

C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 21-Jul-2000

C;Accession: B71176

R;Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Hino, Y.; Yamamoto, S.; Sek

M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudo, N.; Oguc

DNA Res. 5, 55-76, 1998

A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic

A;Reference number: A71000; MUID:98344137; PMID:9679194

A;Accession: B71176

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-160 <KAW>

A;Cross-references: GB:AP000007; NID:93236134; PIDN:BAA30801.1; PID:93258118

A;Experimental source: strain Of3

A;Note: this accession replaces an interim accession for a sequence replaced by GenBan

C;Genetics:

A;Gene: PH1689

C;Superfamily: Pyrococcus horikoshii hypothetical protein PH1689

C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 03-Jun-2002

Qy 61 ENPALLRWAYARTINYVNFRPPKNSLNGALCGFPKPIFYVYIKTERDRKEKLIQGK 120

Db 61 ENPALLRWAYARTINYVNFRPPKNSLNGALCGFPKPIFYVYIKTERDRKEKLIQGK 120

C;Species: Bos primigenius taurus (cattle)

C;Accession: S28237

R;Walker, J. B.; Arizmendi, J. M.; Dupuis, A.; Pearnley, I. M.; Finel, M.; Meda, S. M.; Pilak

J. Mol. Biol. 226, 1051-1072, 1992

A;Title: Sequences of 20 subunits of NADH: ubiquinone oxidoreductase from bovine heart

A;Reference number: S28237; MUID:92389317; PMID:1518044

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-129 <WAL>

A;Cross-references: EMBL:Y64898; NID:9113; PIDN:CAA446107.1; PID:gi14

C;Keywords: electron transfer; mitochondrial; NAD; oxidoreductase

C;Accession: S28237

Qy 121 LDRTFHLSY 129

Db 121 LDRTFHLSY 129

C;Species: Gallus gallus (chicken)

C;Accession: A33164

R;Goldberg, G.S.; Kacmarczyk, W.

Gene 121, 391-398, 1992

A;Title: Sequence of a novel chicken genomic DNA fragment that hybridizes to the murin

A;Reference number: JC1395; MUID:9307061; PMID:1355990

A;Accession: JC1395

A;Molecule type: DNA

A;Residues: 1-124 <GO2>

A;Cross-references: GB:MB4354; NID:911948; PIDN:AAAT0191.1; PID:9211949

C;Species: Gallus gallus (chicken)

C;Accession: AE1318

R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeck

D.; Dominguez-Bernal, G.; Duchaude, B.; Durand, L.; Dussurge, O.; Entian, K.D.; Psihi,

D.; Jones, L.M.; Karst, U.

Science 294, 849-852, 2001

A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitouram, A.;

Ok, C.; Schlueter, T.; Simoes, N.; Vazquez-Boland, J.A.; Voss, H.; Wehlan

RESULT 2

Qy S28237

C;Species: Bos primigenius taurus (cattle)

C;Accession: S28237

R;Walker, J. B.; Arizmendi, J. M.; Dupuis, A.; Pearnley, I. M.; Finel, M.; Meda, S. M.; Pilak

J. Mol. Biol. 226, 1051-1072, 1992

A;Title: Sequences of 20 subunits of NADH: ubiquinone oxidoreductase from bovine heart

A;Reference number: S28237; MUID:92389317; PMID:1518044

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-129 <WAL>

A;Cross-references: EMBL:Y64898; NID:9113; PIDN:CAA446107.1; PID:gi14

C;Keywords: electron transfer; mitochondrial; NAD; oxidoreductase

C;Accession: S28237

Qy 131 LDRTFHLSY 130

Db 131 LDRTFHLSY 130

C;Species: Gallus gallus (chicken)

C;Accession: A33164

R;Goldberg, G.S.; Kacmarczyk, W.

Gene 133, 233-235, 1993

A;Title: A chicken genomic DNA fragment that hybridizes to the murine Hox-3.1 homeobox

A;Reference number: JC2003; MUID:94040816; PMID:7901127

A;Accession: JC2003

A;Molecule type: DNA

A;Residues: 1-133 <GO2>

C;Genetics:

A;Gene: ghw

A;Introns: 6/7/3

C;Keywords: homeobox; phosphoprotein; sulipoprotein; transmembrane protein

C;Banding site: sulfate (Tyr) (covalent) (by protein kinase C) #status predicted

C;Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

C;Accession: S28237

Qy 141 LDRTFHLSY 140

Db 141 LDRTFHLSY 140

C;Species: Gallus gallus (chicken)

C;Accession: A33164

R;Goldberg, G.S.; Kacmarczyk, W.

Gene 133, 233-235, 1993

A;Title: A chicken genomic DNA fragment that hybridizes to the murine Hox-3.1 homeobox

A;Reference number: JC2003; MUID:94040816; PMID:7901127

A;Accession: JC2003

A;Molecule type: DNA

A;Residues: 1-133 <GO2>

C;Genetics:

A;Gene: ghw

A;Introns: 6/7/3

C;Keywords: homeobox; phosphoprotein; sulipoprotein; transmembrane protein

C;Banding site: sulfate (Tyr) (covalent) (by protein kinase C) #status predicted

C;Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

C;Accession: S28237

Qy 151 LDRTFHLSY 150

Db 151 LDRTFHLSY 150

C;Species: Gallus gallus (chicken)

C;Accession: A33164

R;Goldberg, G.S.; Kacmarczyk, W.

Gene 133, 233-235, 1993

A;Title: A chicken genomic DNA fragment that hybridizes to the murine Hox-3.1 homeobox

A;Reference number: JC2003; MUID:94040816; PMID:7901127

A;Accession: JC2003

A;Molecule type: DNA

A;Residues: 1-133 <GO2>

C;Genetics:

A;Gene: ghw

A;Introns: 6/7/3

C;Keywords: homeobox; phosphoprotein; sulipoprotein; transmembrane protein

C;Banding site: sulfate (Tyr) (covalent) (by protein kinase C) #status predicted

C;Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

C;Accession: S28237

Qy 161 LDRTFHLSY 160

Db 171 LDRTFHLSY 160

C;Species: Gallus gallus (chicken)

C;Accession: A33164

R;Goldberg, G.S.; Kacmarczyk, W.

Gene 133, 233-235, 1993

A;Title: A chicken genomic DNA fragment that hybridizes to the murine Hox-3.1 homeobox

A;Reference number: JC2003; MUID:94040816; PMID:7901127

A;Accession: JC2003

A;Molecule type: DNA

A;Residues: 1-133 <GO2>

C;Genetics:

A;Gene: ghw

A;Introns: 6/7/3

C;Keywords: homeobox; phosphoprotein; sulipoprotein; transmembrane protein

C;Banding site: sulfate (Tyr) (covalent) (by protein kinase C) #status predicted

C;Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

C;Accession: S28237

Qy 171 LDRTFHLSY 170

Db 171 LDRTFHLSY 170

C;Species: Gallus gallus (chicken)

C;Accession: A33164

R;Goldberg, G.S.; Kacmarczyk, W.

Gene 133, 233-235, 1993

A;Title: A chicken genomic DNA fragment that hybridizes to the murine Hox-3.1 homeobox

A;Reference number: JC2003; MUID:94040816; PMID:7901127

A;Accession: JC2003

A;Molecule type: DNA

A;Residues: 1-133 <GO2>

C;Genetics:

A;Gene: ghw

A;Introns: 6/7/3

C;Keywords: homeobox; phosphoprotein; sulipoprotein; transmembrane protein

C;Banding site: sulfate (Tyr) (covalent) (by protein kinase C) #status predicted

C;Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

C;Accession: S28237

Qy 181 LDRTFHLSY 180

Db 181 LDRTFHLSY 180

C;Species: Gallus gallus (chicken)

C;Accession: A33164

R;Goldberg, G.S.; Kacmarczyk, W.

Gene 133, 233-235, 1993

A;Title: A chicken genomic DNA fragment that hybridizes to the murine Hox-3.1 homeobox

A;Reference number: JC2003; MUID:94040816; PMID:7901127

A;Accession: JC2003

A;Molecule type: DNA

A;Residues: 1-133 <GO2>

C;Genetics:

A;Gene: ghw

A;Introns: 6/7/3

C;Keywords: homeobox; phosphoprotein; sulipoprotein; transmembrane protein

C;Banding site: sulfate (Tyr) (covalent) (by protein kinase C) #status predicted

C;Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

C;Accession: S28237

Qy 191 LDRTFHLSY 190

Db 191 LDRTFHLSY 190

C;Species: Gallus gallus (chicken)

C;Accession: A33164

R;Goldberg, G.S.; Kacmarczyk, W.

Gene 133, 233-235, 1993

A;Title: A chicken genomic DNA fragment that hybridizes to the murine Hox-3.1 homeobox

A;Reference number: JC2003; MUID:94040816; PMID:7901127

A;Accession: JC2003

A;Molecule type: DNA

A;Residues: 1-133 <GO2>

C;Genetics:

A;Gene: ghw

A;Introns: 6/7/3

C;Keywords: homeobox; phosphoprotein; sulipoprotein; transmembrane protein

C;Banding site: sulfate (Tyr) (covalent) (by protein kinase C) #status predicted

C;Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

C;Accession: S28237

Qy 201 LDRTFHLSY 200

Db 201 LDRTFHLSY 200

C;Species: Gallus gallus (chicken)

C;Accession: A33164

R;Goldberg, G.S.; Kacmarczyk, W.

Gene 133, 233-235, 1993

A;Title: A chicken genomic DNA fragment that hybridizes to the murine Hox-3.1 homeobox

A;Reference number: JC2003; MUID:94040816; PMID:7901127

A;Accession: JC2003

A;Molecule type: DNA

A;Residues: 1-133 <GO2>

C;Genetics:

A;Gene: ghw

A;Introns: 6/7/3

C;Keywords: homeobox; phosphoprotein; sulipoprotein; transmembrane protein

C;Banding site: sulfate (Tyr) (covalent) (by protein kinase C) #status predicted

C;Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

C;Accession: S28237

Qy 211 LDRTFHLSY 210

Db 211 LDRTFHLSY 210

C;Species: Gallus gallus (chicken)

C;Accession: A33164

R;Goldberg, G.S.; Kacmarczyk, W.

Gene 133, 233-235, 1993

A;Title: A chicken genomic DNA fragment that hybridizes to the murine Hox-3.1 homeobox

A;Reference number: JC2003; MUID:94040816; PMID:7901127

A;Accession: JC2003

A;Molecule type: DNA

A;Residues: 1-133 <GO2>

C;Genetics:

A;Gene: ghw

A;Introns: 6/7/3

C;Keywords: homeobox; phosphoprotein; sulipoprotein; transmembrane protein

C;Banding site: sulfate (Tyr) (covalent) (by protein kinase C) #status predicted

C;Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

C;Accession: S28237

Qy 221 LDRTFHLSY 220

Db 221 LDRTFHLSY 220

C;Species: Gallus gallus (chicken)

C;Accession: A33164

R;Goldberg, G.S.; Kacmarczyk, W.

Gene 133, 233-23

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 29, 2004, 09:12:47 ; Search time 17 Seconds
(without alignments)
356.850 Million cell updates/sec

Title: US-09-726-899-3

Sequence: 1 MSRPKYKESSSLRLTIPETLDP.....DRKEKLIQEKGKLDRTFHLSY 129

Perfect score: 129

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 0

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing First 75 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Match	Length	DB ID	Description
1	128	99.2	128	1 NB5M_HUMAN	095168 homo sapien
2	117	13.2	128	1 NB5M_BOVIN	P48305 bos taurus
3	8	6.2	133	1 NB5M_CHICK	P48306 gallus gallus
4	8	6.2	466	1 SELA_RHIME	P58226 rhizobium m
5	8	6.2	468	1 SELA_PSEAL	Q9hv01 pseudomonas
6	8	6.2	1440	1 SYEP_HUMAN	P07814 homo sapien
7	7	5.4	127	1 CRCB_YERPE	Q8zdh2 yersinia pe
8	7	5.4	277	1 PYR2_ANAPSP	P31329 anaerena sp
9	7	5.4	398	1 HUSX_SUTISO	Q33775 sulfolobus
10	7	5.4	532	1 NADD_RHIME	Q92r32 rhizobium m
11	7	5.4	536	1 CAR9_HUMAN	Q9h257 homo sapien
12	7	5.4	577	1 DCPEP_ASPPA	P51844 aspergillus
13	7	5.4	587	1 DHSB_COXBLU	P51054 coxiella bu
14	7	5.4	608	1 ATOS_ECOLI	P06067 escherichia
15	7	5.4	628	1 PTH3_SYNYY3	P73437 synechocystis
16	7	5.4	748	1 SM5B_MOUSE	Q62177 mus musculus
17	7	5.4	967	1 SYL_PYRAB	Q9v0b9 pyrococcus
18	7	5.4	967	1 GLUC_PLATE	P518698 pyrococcus
19	6	4.7	29	1 YAC2_LIEGPNU	P23062 platioblytus
20	6	4.7	57	1 GLUC_ICMPU	P37034 legionella
21	6	4.7	71	1 GLU2_LOPAM	P04093 ictalurus p
22	6	4.7	80	1 CGAL_LUPAN	P09331 lupinus ang
23	6	4.7	93	1 YOFV_BACSU	P49779 bacillus su
24	6	4.7	96	1 GLUC_MYOSC	P09585 myoxocephalus
25	6	4.7	99	1 YL13_ARCPU	Q28167 archaeoglob
26	6	4.7	117	1 VATG_DROM	Q9xz66 drosophila
27	6	4.7	121	1 GLUC_CARABU	P79695 carassius a
28	6	4.7	122	1 GLU2_LOPAM	P04092 lophius aeneus
29	6	4.7	123	1 RRFL_ARCPU	P49501 odontella s
30	6	4.7	123	1 VMAT_VHSAW0	P271663 viral hemor
31	6	4.7	135	1 NUSB_CLOBL	Q8xjd6 clostridium
32	6	4.7	144	1 ARCO_RHIO	Q98ncl rhizobium l
33	6	4.7	150	1 SP18_DRMOC	Q9vex9 drosophila

ALIGNMENTS

RESULT 1	NB5M_HUMAN	STANDARD;	PRT;	128 AA.
ID	NB5M_HUMAN			
AC	095168;			
DT	15-JUL-1999	(Rel. 38, Created)		
DT	15-JUL-1999	(Rel. 38, Last sequence update)		
DT	15-SEP-2003	(Rel. 42, Last annotation update)		
DE	NADH-ubiquinone oxidoreductase B15 subunit (EC 1.6.5.3) (EC 1.6.99.3)			
DE	(Complex I-B15) (CI-B15).			
GN	NDUFBA4.			
RP	SEQUENCE FROM N.A.			
RP	Hom sapiens (Human)			
RP	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;			
RP	Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OC	SEQUENCE FROM N.A.			
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OC	NCBI_TaxID=9606;			
RN	[1]			

SEQUENCE FROM N.A.				
RX	Medline=99097250;	PubMed=9878551;		
RA	Loeffen J.L.C.M., Triepels R.H., van den Heuvel L., Schuelke M.,			
RA	Buskens C.A.F., Smeets R.J.P., Trijbels J.M.F., Smeitink J.A.M.;			
RA	"CDNA of eight nuclear encoded subunits of NADH:ubiquinone			
RT	oxidoreductase: human complex I CDNA characterization completed."			
RT	Biochem. Biophys. Res. Commun. 253:415-422 (1998).			
RL	[2]			
RN				
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Cervix;			
RC	Medline=22388257;	PubMed=12477932;		

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OM protein - protein search, using sw model

Run on: January 29, 2004, 09:13:22 ; Search time 35 Seconds
(without alignments)
951.108 Million cell updates/sec

Title: US-09-726-899-3

Perfect score: 129
Sequence: 1 MSFPKYKPFSSRLTLPETLDP.....DRKEKLIQBGKLDRTFHLSY 129

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size :

0

Total number of hits satisfying chosen parameters:

830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 75 summaries

Database :

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rabbit:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteria:*
- 17: sp_archaea:*

Prev. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	108	83.7	119	4	Q8N4D3	Q8n4d3 homo sapien
2	12	9.3	119	11	Q9DBH2	Q9dbh2 mus musculu
3	12	9.3	129	11	Q9CQ7	Q9cq7 mus musculu
4	8	6.2	160	17	Q9313	Q9313 pyrococcus
5	8	6.2	244	16	Q92A59	Q92a59 listeria in
6	8	6.2	244	16	Q8Y5V6	Q8y5v6 listeria mo
7	8	6.2	345	17	Q8TSM5	Q8tsm5 methanobarc
8	8	6.2	435	16	Q8DCY9	Q8dcy9 vibrio vuln
9	8	6.2	451	16	Q9RNN2	Q9rnn2 vibrio chol
10	8	6.2	658	17	Q74798	Q74798 schizosacch
11	8	6.2	1022	11	Q8CGC7	Q8cgc7 mus musculu
12	7	5.4	88	16	Q8Y2S6	Q8y2s6 ralstonia s
13	7	5.4	102	11	Q8C3A8	Q8c3a8 mus musculu
14	7	5.4	120	5	Q8T539	Q8t539 plasmidium
15	7	5.4	120	5	Q77180	Q77180 plasmidium
16	7	5.4	174	11	Q8BP01	Q8bp01 mus musculu

Q8v5P7 helicoverpa
Q99g8 helicoverpa
Q91b9 helicoverpa
Q9r15 streptomyce
Q9716 caenorhabdi
Q82106 yersinia pe
Q8ckh8 yersinia pe
Q931a8 rhizobium m
Q8aw63 encephalitozoon
Q8ad96 pseudomonas
Q8yvps anabena sp
Q8tpd8 methanosa
Q9zbx0 streptomyce
Q9pdko xylella fast
Q8ljp7 plasmidium
Q8lwd8 oryza sativa
Q85914 sphingomon
Q8fjp8 arabidopsis
Q8a414 caulobacter
Q23568 caenorhabdi
Q92tg8 rhizobium m
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Result No.	Score	Query	Match	Length	DB ID	Description
1	129	GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.	100.0	129	19	AAW69225
2	95	OM protein - protein search, using sw model	73.6	113	20	AYY76229
3	90	Run on: January 29, 2004, 09:09:42 ; Search time 41 Seconds (without alignments) Perfect score: 129 Sequence: 1 MSFPKYKPPSSLRLTPETLDP.....DRKEKLHQEGKLDRTPHLSY 129	69.8	117	23	ABP42296
4	49	Scoring table: Oligo Gapext 60.0 , Gapext 60.0	38.0	68	22	ABG22382
5	41	Scored: 1107863 seqs, 158726573 residues	31.8	294	22	ABB12440
6	24	Word size : 0	18.6	33	22	ABG7202
7	14	Total number of hits satisfying chosen parameters: 1107863	10.9	119	22	AAU33022
8	11	Minimum DB seq length: 0	8.5	16	21	AAB53504
9	8	Maximum DB seq length: 2000000000	6.2	115	22	AAU33023
Post-processing: Listing first 75 summaries						
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24:	/SIDS1/gcggdata/geneseqp-emb1/AA2003.DAT;*					
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.						
SUMMARIES						
1	129	Human bone marrow	8	6	22	ABB12358
2	95	Listeria monocytog	6.2	23	ABB49985	
3	90	Human olfactory re	6.2	22	AAG71925	
4	49	Protein encoded by	6.2	23	AAB47786	
5	41	Human protein SEQ	6.2	22	AAM76732	
6	24	Mammalian toxicolo	6.2	22	AAM03349	
7	14	Human protein SEQ	6.2	22	AAM76716	
8	11	Human secreted pro	5.4	21	AAB6145	
9	8	S. murrayanensis A	5.4	21	ABP51640	
Perfect score: 129						
Sequence: 1 MSFPKYKPPSSLRLTPETLDP.....DRKEKLHQEGKLDRTPHLSY 129						
Title: US-09-726-899-3						
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Searched: 1107863 seqs, 158726573 residues						
Word size : 0						
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.						
SUMMARIES						
1	129	Human ovarian anti	129	19	AAW69225	
2	95	Aspergillus oryzae	6.2	22	AAB49985	
3	90	Human secreted pro	6.2	22	AAG71925	
4	49	C. albicans BAX as	6.2	22	AAB47786	
5	41	Human protein SEQ	6.2	22	AAM76732	
6	24	Human protein SEQ	6.2	22	AAM03349	
7	14	Human protein SEQ	6.2	22	AAM76716	
8	11	Human protein SEQ	5.4	21	AAB6145	
9	8	Human protein SEQ	5.4	21	ABP51640	
Perfect score: 129						
Sequence: 1 MSFPKYKPPSSLRLTPETLDP.....DRKEKLHQEGKLDRTPHLSY 129						
Title: US-09-726-899-3						
Scoring table: Oligo Gapext 60.0 , Gapext 60.0						
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.						
SUMMARIES						
1	129	Human ovarian anti	129	19	AAW69225	
2	95	Aspergillus oryzae	6.2	22	AAB49985	
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5	41	Human protein SEQ	6.2	22	AAM76732	
6	24	Human protein SEQ	6.2	22	AAB53504	
7	14	Human protein SEQ	5.4	21	AAB53504	
8	11	Human protein SEQ	5.4	21	AAB53504	
9	8	Human protein SEQ	5.4	21	AAB53504	
Perfect score: 129						
Sequence: 1 MSFPKYKPPSSLRLTPETLDP.....DRKEKLHQEGKLDRTPHLSY 129						
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ID	AAW69225	standard;	Protein;	129 AA.		
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XX	AC					
DT	18-FEB-1999	(first entry)				
DB	NADH dehydrogenase subunit NDS-2.					
XX	KW	NADH dehydrogenase subunit; sympathetic nervous system disease; myopathy;				
XX	KW	nicotinamide-adenine dinucleotide dehydrogenase; cancer; leukaemia;				
XX	KW	immune system disorder; neurodegenerative disease; therapy; NDS-2.				
OS	Homo sapiens.					
PN	WO9831815-A2.					
XX	PA	(INCYT) INCYTE PHARM INC.				
PD	23-JUL-1998.					
XX	PF	17-DEC-1997; 97WO-US23970.				
XX	PR	17-JAN-1997; 97US-0785065.				
XX	PA	WPI; 1998-414112/35.				
XX	DR	N-PSDB; AAV44787.				
PT	Human nicotinamide-adenine di:nucleotide dehydrogenase sub:units -					
PT	useful for, e.g. diagnosis, treatment and prevention of cancer,					
PT	myopathy, immune system disease and neuro:degeneration					
XX	PS	Claim 19; Fig 2; 80pp; English.				
XX	This sequence represents the NADH (reduced nicotinamide-adenine					
CC	dinucleotide) dehydrogenase subunit, NDS-2, of the invention. Cells					
CC	containing the DNA are used to produce the recombinant subunits.					
CC	Antagonists of NDS-1 (typically antisense sequences or ribozymes) are					
CC	used to treat or prevent cancer (leukaemia and solid cancers) and immune					
CC	osteoporosis and many others); diabetes, rheumatoid arthritis,					
CC	(e.g. ophthalmoplegia, myoclonic epilepsy and lactic acidosis), while					
CC	their antagonists are used to treat cancer and disease of the sympathetic					
CC	nervous system (e.g. hypertension, arrhythmia and migraine); NDS-3 is					
CC	also used to treat myopathy and its antagonists to treat cancer and					
CC	neurodegenerative disease (e.g. Alzheimer's, Huntington's and Parkinson's					
CC	diseases, epilepsy and Down's syndrome). In all cases NDS or their					
CC	antagonists may be expressed from gene therapy vectors. Ab may be used					
CC	therapeutically as antagonists as immunosassay reagent for diagnosis or					
CC	monitoring such diseases; in competitive screening assays for agents that					
CC	bind specifically to the subunits, and for affinity purification of the					
CC	subunits from natural sources. The DNAs are useful as primers and probes					
CC	for diagnosis and monitoring (including detecting predisposition to					
CC	cancer); for gene mapping or identifying related sequences, while the					
CC	subunits are also used to raise antibodies and to screen for specific					
CC	binding agents.					
XX	Sequence	129 AA;				
SQ	Query Match	100.0%;	Score	129;	DB 19;	Length 129;
	Best Local Similarity	100.0%;	Pred. No.	1.2e-129;	2.3e-93;	
	Matches	129;	Conservative	0;	Mismatches	0;
					Indels	0;
					Gaps	0;
Qy	1	MSPPKYKSSLRLPTLPDAENISPETRAQERLAIQKREYLQYNDPNRGLI	60			
Db	1	MSPPKYKSSLRLPTLPDAENISPETRAQERLAIQKREYLQYNDPNRGLI	60			
Qy	61	ENPALLRWAYARTINYVPNFRTPKNSLMLGALCQGPFLIPIYTIKTERKELIQECK	120			
Db	61	ENPALLRWAYARTINYVPNFRTPKNSLMLGALCQGPFLIPIYTIKTERKELIQECK	120			
Qy	95	FGPLIPIYIILKTBDRKEKLQEGFLDRPHLSY	129			
Db	79	FGPLIPIYIILKTBDRKEKLQEGFLDRPHLSY	113			
Qy	35	ERLARAOQLKREYLQYNDPNRGLIENPALLRWAYARTINYVPNFRTPKNSLMLGALC	94			
Db	19	ERLARAOQLKREYLQYNDPNRGLIENPALLRWAYARTINYVPNFRTPKNSLMLGALC	78			

CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp://wipo.int/pub/published_pct_sequences.

SQ Sequence 68 AA;
 Query Match 61 ENPALLRWARTINYVNFRTPPKNSIMGALCGFPDIFTYIITKTR 109
 Best Local Similarity 100.0%; Score 49; DB 22; Length 68;
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 9 ENPALLRWARTINYVNFRTPPKNSIMGALCGFPDIFTYIITKTR 57

RESULT 5

ABB12440

ID ABB12440 standard; Protein; 294 AA.

XX XX

AC ABB12440;

XX DT 15-JAN-2002 (first entry)

XX DE Human bone marrow expressed protein SEQ ID NO: 279.

XX KW Human; bone marrow; cytostatic; antiarthritic; antiarthritic; vulnerary;

KW antiinflammatory; antibacterial; immunosuppressive; vasoconstrictor; cancer;

KW antiparkinsonian; neuroprotective; motropic; hemostatic; osteopathic;

KW antilulcer; fungicide; antidiabetic; antiasthmatic; antiallergic;

KW immunostimulant; analgesic; cerebroprotective; antianemic; infection;

KW nervous system disorder; autoimmune disorder; inflammation; allergy.

OS Homo sapiens.

XX PN WO200174836-A1.

XX PD 11-OCT-2001.

XX XX

PP 30-MAR-2001; 2001WO-US10472.

XX XX 31-MAR-2000; 2000US-0540217.

PR 23-AUG-2000; 2000US-0649167.

PR 23-AUG-2000; 2000US-0649267.

PR 30-NOV-2000; 2000US-220583P.

XX XX

PA (HYSE-) HYSEQ INC.

PA XX

PT Tang YT, Liu C, Drmanac RT, Ford JE, Boyle BJ;

PT XX

PR WPI; 2001-626375/72.

PR DR

XX PS 10; Page 331; 380pp; English.

XX XX

PT The present invention relates to bone marrow expressed polynucleotides

PT and proteins. These sequences can be used in the treatment of

PT inflammatory conditions (eg arthritis, Crohn's disease),

PT and increasing hematopoiesis, stem cell survival and bone growth and

PT remodeling.

XX PS Claim 10; Page 331; 380pp; English.

XX XX

PT The present invention relates to bone marrow expressed polynucleotides

PT and proteins. These sequences can be used in the treatment of

PT inflammatory conditions (eg arthritis, Crohn's disease),

PT and peripheral nervous system diseases and neuropathies, such as

PT Alzheimer's, Parkinson's and Huntington's diseases, spinal cord

PT cell disorders, head trauma, cerebrovascular diseases, myeloid and lymphoid

PT degenerative disorders, platelet disorders, stem cell disorders, bone

PT scleriosis, diabetes and arthritis, viral and bacterial infections,

PT allergies and blood coagulation disorders. The present sequence is a

PT protein of the invention.

SQ Sequence 294 AA;

Query Match 31.8%; Score 41; DB 22; Length 294;

Best Local Similarity 100.0%; Pred. No. 2.8e-35;
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 40 RAQLKREYLQYNDPQRGLIENPALARWARTINYVNPNF 80

Db 119 RAQLKREYLQYNDPQRGLIENPALARWARTINYVNPNF 159

RESULT 6

AAG73633 standard; Protein; 33 AA.

XX XX

AC AAG73633;

XX XX

DT 03-SEP-2001 (first entry)

XX XX

DE Human colon cancer antigen protein SEQ ID NO:4397.

XX XX

Human; colon cancer; colon cancer antigen; diagnosis; detection; colorectal carcinoma.

XX XX

Homo sapiens.

XX XX

WO200122920-A2.

XX XX

PD 05-APR-2001.

XX XX

28-SEP-2000; 2000WO-US26524.

XX XX

29-SEP-1999; 99US-0157137.

XX PR 03-NOV-1999; 99US-0163280.

XX XX

(HUMA-) HUMAN GENOME SCI INC.

XX XX

Ruben SM, Barash SC, Birse CB, Rosen CA;

XX XX

WPI; 2001-2335357/24.

DR N-PSDB; AAH33064.

XX XX

Nucleic acids encoding 4277 human colon cancer-associated polypeptides,

PT useful for preventing, diagnosing and/or treating colorectal cancers -

XX XX

Claim 11; Page 6222-6223; 9803PP; English.

XX XX

AAH32943 to AAH7195 and AAH73514 to AAG7788 represent human colon

CC cancer-associated nucleic acid molecules (N) and proteins (P), where

CC the proteins are collectively known as colon cancer antigens. The colon

CC cancer antigens have cytostatic activity and can be used in gene

CC therapy and vaccine production. N and P may be used in the prevention,

CC diagnosis and treatment of diseases associated with inappropriate P

CC expression. For example, N and P may be used to treat disorders

CC associated with decreased expression by rectifying mutations or deletions

CC in a patient's genome that affect the activity of P by expressing

CC inactive proteins or to supplement the patient's own production of P.

CC Additionally, N may be used to produce the colon cancer-associated Ps,

CC by inserting the nucleic acids into a host cell and culturing the cell

CC to express the proteins. N and P can be used in the prevention, diagnosis

CC and treatment of colorectal carcinomas and cancers, AAH37204

CC and AAH7789 represent sequences used in the exemplification of the

CC present invention.

CC Pages 66 to 682 and page 7053 of the sequence listing were

CC missing at time of publication, meaning no sequences are present for

CC SEQ ID NO:1027 to 1052, 7921 and 7922.

CC N.B. Pages 66 to 682 and page 7053 of the sequence listing were

CC present invention.

CC Sequence 33 AA;

SQ Query Match 18.6%; Score 24;

Best Local Similarity 100.0%; Pred. No. 5.8e-18;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 106 KTEDRKEKLIQSGLDRTFLSY 129

Db 10 KTEDRKEKLIQSGLDRTFLSY 33

DT	09-MAR-2001	(First entry)
XX	Human colon cancer antigen protein sequence SEQ ID NO:1044.	
DB	AAU33022 standard; Protein; 119 AA.	
XX	Human; colon cancer; colon cancer antigen; diagnosis; detection; identification; cytotoxic; cardioactive; immunomodulatory; nephrotoxic; neural disorder; reproductive disorder; infectious disease; cardiovascular disorder.	
XX	Human; vaccination; gene therapy; nutritional supplement; stem cell proliferation; haemopoiesis; nerve tissue regeneration; immune suppression; immune stimulation; anti-inflammatory; leukaemia.	
OS	Homo sapiens.	
XX	WO20055351-A1.	
XX	WO2000055351-1A1.	
XX	PD 21-SEP-2000.	
XX	PF 08-MAR-2000; 2000WO-US05883.	
XX	PR 12-MAR-1999; 99US-0124270.	
XX	PA (HUMA-) HUMAN GENOME SCI INC.	
XX	Colon cancer associated gene sequences, referred to as colon cancer antigens, useful for the treatment, prevention, and diagnosis of colon disorders such as colon cancer -	
XX	Claim 11; Page 1624; 2104pp; English.	
XX	AAC9791 to AAC98763 encode the human colon cancer associated proteins, called human colon cancer antigens. Given in AAC9791 to AAC98763. The human colon cancer antigens can have cytotoxic, cardioactive, muscular, neuroprotective, immunomodulatory, gynaecological, gastrointestinal, nephrotoxic, antiinfective and antibacterial activities, and can be used in gene therapy. The colon cancer antigen polynucleotides, proteins and antibodies to the proteins are useful for the prevention, treatment and diagnosis of colon disorders, such as colon cancer. The polynucleotides may be used in diagnostics and research, such as for chromosome identification, and as hybridisation probes. The proteins may also be used to prevent diseases such as neural disorders, immune system disorders, muscular disorders, reproductive disorders, gastrointestinal disorders, wounds, renal disorders, infectious diseases, and cardiovascular disorders. AAC98764 to AAC98772 and AAC98773 represent sequences used in the exemplification of the present invention.	
XX	Sequence 16 AA;	
XX	Query Match 8.5%; Score 11; DB 21; Length 16;	
XX	Best Local Similarity 100.0%; Pred. No. 0.00003; Mismatches 0; Indels 0; Gaps 0;	
Qy	119 GKLDRTFHLSY 129	
Db	6 GKLDRTFHLSY 16	
RESULT 9		
ID	AAU33023	
XX	AAU33023 standard; Protein; 115 AA.	
AC	AAU33023;	
XX		
DT	18-DEC-2001	(First entry)
XX	Novel human secreted protein #3513.	
XX	Tang YT, Liu C, Drmanac RT;	
XX	WPI; 2001-611725/70.	
XX	Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy -	
XX	Claim 20; Page 699; 765pp; English.	
XX	The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising the nucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and therapy, and can be used as nutritional supplements. They may be used to increase stem cell proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or stimulation; as anti-inflammatory agents; and in treatment of leukaemias. ABU2951-0-AAU33304 represent the amino acid sequences of novel human secreted proteins of the invention.	
XX	Sequence 119 AA;	
XX	Query Match 10.9%; Score 14; DB 22; Length 119;	
XX	Best Local Similarity 100.0%; Pred. No. 8.8e-07; Mismatches 0; Indels 0; Gaps 0;	
Qy	75 NVPNNFRPTPNSL 88	
Db	71 NVPNNFRPTPNSL 84	
RESULT 8		
ID	AAB53504	
XX	AAB53504 standard; Protein; 16 AA.	
AC	AAB53504;	
XX		
DT	18-DEC-2001	(First entry)
XX	Novel human secreted protein #3514.	

KW Human; vaccination; gene therapy; nutritional supplement;
 KW stem cell proliferation; haemopoiesis; nerve tissue regeneration;
 KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.
 XX
 XX
 OS Homo sapiens.
 PN WO200179449-A2.
 XX
 XX
 PD 25-OCT-2001.
 XX
 PR 16-APR-2001; 2001WO-US086556.
 XX
 PR 18-APR-2000; 2000US-0552929.
 XX
 PR 26-JAN-2001; 2001US-0770160.
 XX
 PA (HYSEQ-) HYSEQ INC.
 XX
 PA Tang YT, Liu C, Drmanac RT, Ford JB, Boyle BJ.
 XX
 XX
 DR WPI; 2001-626375/72.
 DR N-PSDB; ABA09602.
 XX
 PT New bone marrow-expressed nucleic acids and polypeptides, useful for
 PT diagnosis, treatment of inflammatory, autoimmune, neurological, cancer
 PT and increasing hematopoiesis, stem cell survival and bone growth and
 PT remodeling -
 XX
 PS Claim 10; Page 221; 380pp; English.
 XX
 XX
 CC The present invention relates to bone marrow expressed polynucleotides
 CC and proteins. These sequences can be used in the treatment of
 CC inflammatory conditions (eg arthritis, Crohn's disease), cancer, central
 CC and peripheral nervous and neuropathies, such as
 CC Alzheimer's, Parkinson's and Huntington's diseases, spinal cord
 CC disorders, head trauma, cerebrovascular diseases, myeloid and lymphoid
 CC disorders, platelet disorders, stem cell disorders, bone
 CC degenerative disorders, autoimmune disorders, for example, multiple
 CC sclerosis, diabetes and arthritis, viral and bacterial infections,
 CC allergies and blood coagulation disorders. The present sequence is a
 CC protein of the invention.
 XX
 SQ Sequence 155 AA;
 XX
 CC The invention relates to novel human secreted polypeptides. The
 CC polypeptides and antibodies to the polypeptides are useful for
 CC determining the presence of or predisposition to a disease associated
 CC with altered levels of polypeptide. The polypeptides are also useful for
 CC identifying agents (agonists and antagonists) that bind to them. Cells
 CC expressing the proteins are useful for identifying a therapeutic agent
 CC for use in treatment of a pathology related to aberrant expression or
 CC physiological interactions of the polypeptide. Vectors comprising
 CC the nucleic acids encoding the polypeptides and cells genetically
 CC engineered to express them are also useful for producing the proteins.
 CC The proteins are useful in genetic vaccination, testing and
 CC therapy, and can be used as nutritional supplements. They may be used to
 CC increase stem cell proliferation; to regulate haemopoiesis; and in
 CC bone, cartilage, tendon and/or nerve tissue growth or regeneration;
 CC immune suppression and/or stimulation; as anti-inflammatory agents; and
 CC in treatment of leukaemias. AU29510-AAU33304 represent the amino acid
 CC sequences of novel human secreted proteins of the invention.
 XX
 SQ Sequence 115 AA;
 XX
 CC Query Match 6.2%; Score 8; DB 22; Length 115;
 CC Best Local Similarity 100.0%; Pred. No. 2.2;
 CC Matches 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 XX
 AC ABB12358;
 XX
 DT 15-JAN-2002 (first entry)
 XX
 DE Human bone marrow expressed protein SEQ ID NO: 112.
 XX
 ID ABB12358 Standard; Protein; 155 AA.
 XX
 AC ABB12358;
 XX
 DT 15-JAN-2002 (first entry)
 XX
 DE Human bone marrow expressed protein SEQ ID NO: 112.
 XX
 KW Human; bone marrow; cytosatic; antiarthritic; antirheumatic; vulnerable;
 KW antiinflammatory; antibacterial; immunosuppressive; vasotropic; cancer;
 KW antiparkinsonian; neuroprotective; notropic; haemostatic; osteopathic;
 KW antiulcer; fungicide; antidiabetic; antiasthmatic; antiallergic;
 KW immunostimulant; analgesic; cerebroprotective; antitanaemic; infection;
 KW nervous system disorder; autoimmune disorder; inflammation; allergy.
 XX
 OS Homo sapiens.
 XX
 PN WO200174836-A1.
 XX
 PD 11-OCT-2001.
 XX
 PR 30-MAR-2001; 2001WO-US10472.
 XX
 PR 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-064167.
 PR 23-AUG-2000; 2000US-064267.
 PR 30-NOV-2000; 2000US-250583P.
 XX
 PA (HYSEQ-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Drmanac RT, Ford JB, Boyle BJ;
 XX
 DR WPI; 2001-626375/72.
 DR N-PSDB; ABA09602.
 XX
 PT New bone marrow-expressed nucleic acids and polypeptides, useful for
 PT diagnosis, treatment of inflammatory, autoimmune, neurological, cancer
 PT and increasing hematopoiesis, stem cell survival and bone growth and
 PT remodeling -
 XX
 PS Claim 10; Page 221; 380pp; English.
 XX
 XX
 CC The present invention relates to bone marrow expressed polynucleotides
 CC and proteins. These sequences can be used in the treatment of
 CC inflammatory conditions (eg arthritis, Crohn's disease), cancer, central
 CC and peripheral nervous and neuropathies, such as
 CC Alzheimer's, Parkinson's and Huntington's diseases, spinal cord
 CC disorders, head trauma, cerebrovascular diseases, myeloid and lymphoid
 CC disorders, platelet disorders, stem cell disorders, bone
 CC degenerative disorders, autoimmune disorders, for example, multiple
 CC sclerosis, diabetes and arthritis, viral and bacterial infections,
 CC allergies and blood coagulation disorders. The present sequence is a
 CC protein of the invention.
 XX
 SQ Sequence 155 AA;
 XX
 CC Query Match 6.2%; Score 8; DB 22; Length 155;
 CC Best Local Similarity 100.0%; Pred. No. 2.9;
 CC Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 XX
 AC ABB48985;
 XX
 DT 05-FEB-2002 (first entry)
 XX
 DE Listeria monocytogenes protein #1689.
 XX
 ID ABB48985 Standard; Protein; 244 AA.
 XX
 AC ABB48985;
 XX
 DT 05-FEB-2002 (first entry)
 XX
 DE Listeria monocytogenes.
 XX
 PN WO200177335-A2.
 XX
 PR 18-OCT-2001.
 XX
 PR 11-APR-2001; 2001WO-FR0118.
 XX
 PR 11-APR-2000; 2000FR-0004629.
 XX
 PA (INSP) INST PASTEUR.

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OM protein - protein search, using SW model

Run on: January 29, 2004, 09:17:12 ; Search time 33 Seconds

(without alignment) 812.403 Million cell updates/sec

Title: US-09-726-899-3

Perfect score: 129

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Sequence: 1 MSFPKYKPSLRLTLPETLDP.....DRKEKLIQEGKUDRTTFHL-SY 129

Score: 789580

Seqs: 207824079 residues

Word size : 0

Total number of hits satisfying chosen parameters: 789580

Minimum DB seq length: 0

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Post-processing: Listing first 75 summaries

Database : Published Applications AA:*

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12: /cgmn_6/prodata/1/pubpaas/US09_NEW_PUBCOMB.pep:*

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18: /cgmn_6/prodata/1/pubpaas/US60__PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	129	100.0	129 9 US-09-726-899-3	Sequence 3, Appli
2	69.8	117 12 US-10-64-049-3428	Sequence 4428, Appli	
3	24	18.6 33 15 US-10-06-638-4407	Sequence 13444, Appli	
4	17	13.2 129 9 US-09-726-899-10	Sequence 4407, Appli	
5	11	8.5 16 11 US-09-925-299-1044	Sequence 1044, Appli	
6	11	8.5 16 11 US-10-156-761-13444	Sequence 1044, Appli	
7	9	7.0 479 15 US-10-06-638-4407	Sequence 2, Appli	
8	8	6.4 512 12 US-10-132-134-12	Sequence 12, Appli	
9	8	6.2 8026 12 US-10-032-159A-6	Sequence 6, Appli	
10	7	5.4 144 14 US-10-187-267A-65	Sequence 6, Appli	
11	7	5.4 213 9 US-09-925-301-1259	Sequence 2, Appli	
12	7	5.4 247 9 US-10-136-433-17015	Sequence 17015, Appli	
13	7	5.4 366 12 US-10-032-159A-2	Sequence 2, Appli	
14	7	5.4 366 14 US-10-032-159A-20	Sequence 20, Appli	

ALIGMENTS

RESULT 1
US-09-726-899-3
GENERAL INFORMATION:
/ APPLICANT: Bandman, Olga
/ APPLICANT: Goli, Surya K.
/ APPLICANT: Hillman, Jennifer L.

RESULT 1
US-09-726-899-3
GENERAL INFORMATION:
/ Sequence 3, Application US/09726899
/ Sequence No. US2001004135641

Sequence 104, Appli
Sequence 9715, Appli
Sequence 9756, Appli
Sequence 4807, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 2683, Appli
Sequence 3, Appli
Sequence 7964, Appli
Sequence 2, Appli
Sequence 3239, Appli
Sequence 869, Appli
Sequence 31113, A
Sequence 33241, A
Sequence 1098, Appli
Sequence 7255, Appli
Sequence 7978, Appli
Sequence 822, Appli
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Sequence 5241, Appli
Sequence 78, Appli
Sequence 85, Appli
Sequence 9, Appli
Sequence 3335, Appli
Sequence 1919, Appli
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Sequence 6134, Appli
Sequence 219, Appli
Sequence 21, Appli
Sequence 30374, A
Sequence 30175, Appli
Sequence 1047, Appli
Sequence 221, Appli
Sequence 424, Appli
Sequence 21, Appli
Sequence 951, Appli
Sequence 3502, Appli
Sequence 48, Appli
Sequence 29446, A
Sequence 480, Appli
Sequence 31964, A

TITLE OF INVENTION: NOVEL SUBUNITS OF NADH DEHYDROGENASE
 NUMBER OF SEQUENCES: 12
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Incyte Pharmaceuticals, Inc.
 STREET: 3174 Porter Drive
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94304
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/726, 899
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/785, 065
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Billing, Lucy J.
 REFERENCE/DOCKET NUMBER: 36-749
 REFERENCE/DOCKET NUMBER: PP-0187 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-855-0555
 TELEX:
 415-845-4166
 TELEX:
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 129 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: Consensus
 CLONE: Consensus
 US-09-726-899-3

Query Match 100.0%; Score 129; DB 9; Length 129;
 Best Local Similarity 100.0%; Pred. No. 1.3e-119;
 Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSPKPKSSLRLTPETDPAETNISPTRAQERLRAQREYLQYNDPNRGLI 60
 Db 1 MSPKPKSSLRLTPETDPAETNISPTRAQERLRAQREYLQYNDPNRGLI 60

Qy 61 ENPALLRQAYARTINYYNFRPTPKNSLMGALCGFGPPIFYVYIKTERDRKERKLIGQK 120
 Db 61 ENPALLRQAYARTINYYNFRPTPKNSLMGALCGFGPPIFYVYIKTERDRKERKLIGQK 120

Qy 121 LDRTPHLSY 129
 Db 121 LDRTPHLSY 129

RESULT 2
 US-10-264-049-3428
 Sequence 3428, Application US/10264049
 General Information:
 Applicant: Birs, et al.
 Title of Invention: Nucleic Acids, Proteins, and Antibodies
 File Reference: PA133P1
 Current Application Number: US/10/264, 049
 Prior Application Number: PCT/US01/18569
 Prior Filing Date: 2001-06-07
 Prior Application Number: US 60/209, 467
 Prior Filing Date: 2000-06-07
 Number of SEQ ID NOS: 4360
 Software: PatentIn Ver. 3.1

; SEQ ID NO 3428
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (3)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (27)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
US-10-264-049-3428
Query Match 69.8%; Score 90; DB 12; Length 117;
Best Local Similarity 100.0%; Pred. No. 4.1e-81;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 12 RLTLPETDPAETNISPTRAQERLRAQERLRAQREYLQYNDPNRGLIENPALLRWA 87
Db 28 RTIINVPNFRPTPKNSLMGALCGFGPLIFI 101
Qy 72 RTIINVPNFRPTPKNSLMGALCGFGPLIFI 101
Db 88 RTIINVPNFRPTPKNSLMGALCGFGPLIFI 117
RESULT 3
US-10-106-698-4407
Sequence 4407, Application US/10106698
Publication No. US20030109690A1
GENERAL INFORMATION:
APPLICANT: Ruben, et al.
TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypepti
FILE REFERENCE: PA005P1
CURRENT APPLICATION NUMBER: US/10/106, 598
CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: PCT/US00/26524
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US 60/157, 137
PRIOR FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: US 60/163, 280
PRIOR FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 8564
SEQ ID NO 4407
LENGTH: 33
TYPE: PRT
ORGANISM: Homo sapiens
US-10-106-698-4407
Query Match 18.6%; Score 24; DB 15; Length 33;
Best Local Similarity 100.0%; Pred. No. 2.4e-16;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 10 KTERDRKELIQQGKLDRTFHLSY 33
RESULT 4
US-09-726-899-10
Sequence 10, Application US/09726899
Patent No. US20010041356A1
GENERAL INFORMATION:
APPLICANT: Bandman, Olga K.
APPLICANT: Goli, Surya K.
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: NOVEL SUBUNITS OF NADH DEHYDROGENASE
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive

CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94304
 COMPUTER READABLE FORM:
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/726,899
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/785,065
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Billings, Lucy J.
 REGISTRATION NUMBER: 36,749
 REFERENCE/DOCKET NUMBER:
 TELEPHONE: 415-845-0555
 TELEFAX: 415-845-4166
 TELEX:
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 129 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 LIBRARY: Genbank
 CLONE: 114
 US-09-726-899-10

RESULT 5
 US-09-925-299-1044
 / Sequence 1044, Application US/09925299
 / Patent No. US20020055627A1
 / GENERAL INFORMATION:
 / APPLICANT: Rosen et al.
 / TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
 / FILE REFERENCE: PA102
 / CURRENT APPLICATION NUMBER: US/09/925,299
 / CURRENT FILING DATE: 2001-08-10
 / PRIOR APPLICATION NUMBER: PCT/US00/05883
 / PRIOR FILING DATE: 2000-03-08
 / PRIOR APPLICATION NUMBER: 60/124,270
 / PRIOR FILING DATE: 1999-03-12
 / NUMBER OF SEQ ID NOS: 1556
 / SOFTWARE: Patentin Ver. 2.0
 / SEQ ID NO: 1044
 / LENGTH: 16
 / TYPE: PRT
 / ORGANISM: Homo sapiens
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 Db 6 GKLDRTHLSY 16

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 / Sequence 1044, Application US/09925299
 / Publication No. US2003004617A9
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 / APPLICANT: Rosen et al.
 / TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
 / FILE REFERENCE: PA102
 / CURRENT APPLICATION NUMBER: US/09/925,299
 / CURRENT FILING DATE: 2001-08-10
 / PRIOR APPLICATION NUMBER: PCT/US00/05883
 / PRIOR FILING DATE: 2000-03-08
 / PRIOR APPLICATION NUMBER: 60/124,270
 / PRIOR FILING DATE: 1999-03-12
 / NUMBER OF SEQ ID NOS: 1556
 / SOFTWARE: Patentin Ver. 2.0
 / SEQ ID NO: 1044
 / LENGTH: 16
 / TYPE: PRT
 / ORGANISM: Homo sapiens
 US-09-925-299-1044

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RESULT 7
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 / Sequence 13444, Application US/10156761
 / Publication No. US20030119018A1
 / GENERAL INFORMATION:
 / APPLICANT: OMURA, SATOSHI
 / APPLICANT: IKEDA, HARU
 / APPLICANT: ISHIKAWA, JUN
 / APPLICANT: HORIKAWA, HIROSHI
 / APPLICANT: SHIBA, TADAYOSHI
 / APPLICANT: SAKAKI, YOSHIOKI
 / APPLICANT: HATTORI, MASAHIRA
 / TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
 / FILE REFERENCE: 249-262
 / CURRENT APPLICATION NUMBER: US/10/156,761
 / CURRENT FILING DATE: 2002-05-29
 / PRIOR APPLICATION NUMBER: JP 2001-204089
 / PRIOR FILING DATE: 2001-05-30
 / PRIOR APPLICATION NUMBER: JP 2001-272697
 / PRIOR FILING DATE: 2001-08-02
 / NUMBER OF SEQ ID NOS: 15109
 / SEQ ID NO: 13444
 / LENGTH: 479
 / TYPE: PRT
 / ORGANISM: Streptomyces avermitillis
 US-10-156-761-13444

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 Db 242 LPBTLDPAB 250

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 / Publication No. US2003016218A1

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 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 119 GKLDRTHLSY 129
 Db 6 GKLDRTHLSY 16

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; GENERAL INFORMATION:
; APPLICANT: EMALFAR, MARK A.
; APPLICANT: PUNT, PETER J.
; APPLICANT: VAN ZELT, CORNELIA
; APPLICANT: VAN DEN HONDEL, CORNELIUS
; TITLE OF INVENTION: HIGH-THROUGHPUT SCREENING OF EXPRESSED DNA LIBRARIES IN
; TITLE OF INVENTION: FILAMENTOUS FUNGI
; FILE REFERENCE: 3133-4-006
; CURRENT APPLICATION NUMBER: US/09/834,434
; CURRENT FILING DATE: 2003-03-13
; PRIOR APPLICATION NUMBER: PCT/US00/10199
; PRIOR FILING DATE: 2000-04-13
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 2
; LENGTH: 512
; TYPE: PRT
; ORGANISM: Aspergillus niger
; US-09-834-434-2

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Best Local Similarity 100.0%; Pred. No. 15;
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Db 186 PSSRLTPP 193

RESULT 9
US-10-132-114-12
; Sequence 12, Application US/10132134
; GENERAL INFORMATION:
; APPLICANT: Farne, Chris
; APPLICANT: Yang, Xianshu
; APPLICANT: Staffa, Alfredo
; APPLICANT: Zasopoulos, Emmanuel
; TITLE OF INVENTION: POLYKETIDE SYNTHASE ENZYMES
; FILE REFERENCE: 3012-2US
; CURRENT APPLICATION NUMBER: US/10/132,134
; CURRENT FILING DATE: 2002-04-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 12
; LENGTH: 8026
; TYPE: PRT
; ORGANISM: Streptomyces platensis subsp. rosaceus
; US-10-132-114-12

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Qy 30 RRAQAEQL 37
Db 5943 RRAQAEQL 5950

RESULT 10
US-10-032-1159A-6
; Sequence 6, Application US/10032159A
; GENERAL INFORMATION:
; APPLICANT: Pawlowski, Krzysztof
; APPLICANT: Reed, John C.
; APPLICANT: Godzik, Adam
; TITLE OF INVENTION: CARD-DOMAIN CONTAINING POLYPEPTIDES,
; TITLE OF INVENTION: ENCODING NUCLEIC ACIDS, AND METHODS OF USE
; FILE REFERENCE: P-LJ 5100
; CURRENT APPLICATION NUMBER: US/10/032,159A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: US 60/257,457

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Best Local Similarity 100.0%; Pred. No. 52;
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Db 116 QEQSKLDR 122

RESULT 11
US-10-187-267A-65
; Sequence 65, Application US/10187267A
; Publication No. US20030124679A1
; GENERAL INFORMATION:
; APPLICANT: Short, Jay M.
; APPLICANT: Paradkar, Ashish
; APPLICANT: Varoglu, Mustafa
; APPLICANT: Matlur, Eric J.
; TITLE OF INVENTION: GLYCOSYLATED KINAMYCINS AND METHODS OF
; GLYCOSYLATING THEM
; FILE REFERENCE: 09010-261001
; CURRENT APPLICATION NUMBER: US/10/187,267A
; CURRENT FILING DATE: 2003-01-27
; PRIOR APPLICATION NUMBER: US 60/301,401
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO: 65
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Streptomyces murayaensis ATCC 21414
; US-10-187-267A-65

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Qy 16 ETLDPAE 22
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RESULT 12
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; Sequence 1259, Application US/09925301
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925,301
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; NUMBER OF SEQ ID NOS: 1634
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 1259
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE: SITE
; NAME/KEY: SITE

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Best Local Similarity 100.0%; Pred. No. 72;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 39 ETLDPAE 45

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OM protein - protein search, using sw mode1

Run on: January 29, 2004, 09:14:57 ; Search time 21 Seconds

(without alignments)
259.910 Million cell updates/sec

Title: US-09-726-899-3

Perfect score: 129

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Searched: 328717 seqs, 42310858 residues

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Total number of hits satisfying chosen parameters:

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 75 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARES

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2	129	100.0	129	4 US-09-151-412-3
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4	17	13.2	129	4 US-09-151-412-10
5	8	6.2	1112	4 US-09-252-991A-7256
6	8	6.2	1440	3 US-09-357-251-37
7	8	6.2	1512	4 US-09-443-184-48
8	7	5.4	301	4 US-09-252-991A-78663
9	7	5.4	449	2 US-08-819-458A-16
10	7	5.4	455	4 US-09-252-991A-22154
11	7	5.4	636	2 US-08-871-266B-2
12	7	5.4	636	2 US-08-819-458A-2
13	7	5.4	636	2 US-09-018-864A-2
14	7	5.4	636	3 US-08-871-267B-2
15	7	5.4	636	3 US-09-618-419-2
16	7	5.4	3170	3 US-09-036-87A-4
17	7	5.4	636	2 US-09-370-700-4
18	7	5.4	3170	4 US-09-603-207-4
19	7	5.4	4150	3 US-09-428-517-2
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21	6	4.7	15	1 US-08-231-575-30
22	6	4.7	15	5 PCT-US93-06928-30
23	6	4.7	16	2 US-08-675-921B-6
24	6	4.7	36	6 US-08-836-528-1
25	6	4.7	83	4 US-09-198-452A-11
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Result No.	Query Score	Match Length	DB ID	Description
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3	17	2	US-08-785-065-10	Sequence 10, Appli
4	17	4	US-09-151-412-10	Sequence 10, Appli
5	8	4	US-09-252-991A-7256	Sequence 2726, A
6	8	6.2	US-09-357-251-37	Sequence 37, Appli
7	8	6.2	US-09-443-184-48	Sequence 48, Appli
8	7	5.4	US-09-252-991A-78663	Sequence 16, Appli
9	7	5.4	US-08-819-458A-16	Sequence 16, Appli
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11	7	5.4	US-08-871-266B-2	Sequence 2, Appli
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15	7	5.4	US-09-618-419-2	Sequence 2, Appli
16	7	5.4	US-09-036-87A-4	Sequence 4, Appli
17	7	5.4	US-09-370-700-4	Sequence 4, Appli
18	7	5.4	US-09-603-207-4	Sequence 6, Appli
19	7	5.4	US-09-428-517-2	Sequence 2, Appli
20	6	4.7	15	1 US-07-918-181A-30
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ALIGMENTS

Sequence 5, Appli

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US-09-732-210-5246

OPERATING SYSTEM: DOS
 SOFTWARE: FastSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/785, 065
 FILING DATE: Herewith
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Billings, Lucy J.
 REGISTRATION NUMBER: 36,749
 REFERENCE/DOCKET NUMBER: PP-0187 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-855-0555
 TELEFAX: 415-845-4166
 TELEX:
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 129 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: Consensus
 CLONE: Consensus
 -08-785-065-3

Query Match 100.0% Score 129; DB 2.0
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SULT 2
 -09-151-412-3
 Sequence 3, Application US/09151412
 Patent No. 639945
 GENERAL INFORMATION:
 APPLICANT: Bandman, Olga
 APPLICANT: Goli, Surya K.
 APPLICANT: Hillman, Jennifer L.
 TITLE OF INVENTION: NOVEL SUBUNITS OF NADH D
 NUMBER OF SEQUENCES: 12
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Incyte Pharmaceuticals, Inc.
 STREET: 3174 Porter Drive
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94304
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/151, 412
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/785, 065

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FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0187 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: Consensus
CLONE: Consensus
US-09-151-412-3

Query Match Score 129; DB 4; Length 129;
Best Local Similarity 100.0%; Pred. No. 5.7e-119;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 ENPALLRWAYARTINYVPNFRPTPKNSLMGALCGFPLIIFYIITKDRKEKLQBGK 120
Db 61 ENPALLRWAYARTINYVPNFRPTPKNSLMGALCGFPLIIFYIITKDRKEKLQBGK 120

Qy 121 LDRTFHLSY 129
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RESULT 3
US-09-785-065-10
Sequence 10, Application US/08785065
; Patent No. 5814451
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: NOVEL SUBUNITS OF NADH DEHYDROGENASE
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0187 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166

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